BIOINFORMATICS, 001 - 032

- ThP 001 Peptide Identification from Mixture Tandem Mass Spectra; Jian Wang¹; Josue Perez¹; Ronald Luethy²; Parag Mallick²; Nuno Bandeira³; ¹Bioinformatics Program, UCSD, San Diego, CA; ²Dept. of Chemistry and Biochemistry, UCLA, Los Angeles, CA; ³Center for Computational Mass Spectrometry, UCSD, San Diego, CA
- ThP 002 RAId_deNovo: Using de novo Statistics to Combine Search Results from Multiple Scoring Functions and More; Gelio Alves; Aleksey Ogurtsov; Yi-kuo Yu; National Center for Biotechnology Information, NLM, Bethesda, MD
- ThP 003 Automated Multiple Round Searches to Increase

 Coverage of Peptide/Protein Identification; Baozhen
 Shan¹; Lei Xin²; Weijie Yang¹; Gilles Lajoie²; Bin Ma³;

 Bioinformatics Solutions Inc., Waterloo, Canada;

 University of Western Ontario, London, ON;

 Juniversity of Waterloo, Waterloo, ON
- ThP 004 HyPep: A New Strategy to Accelerate Peptide
 Discovery with a Combination of de novo
 Sequencing and Homology Database Search;
 Weifeng Cao¹; Mingming Ma²; Qiang Fu³; Lingjun Li⁴;

 ¹University of Wisconsin-Madison, Madison, WI;

 ²University of Wisconsin-Madison, Madison, WI;

 ³Schering Plough, North Plainfield, NJ; ⁴University of Wisconsin, Madison, WI
- ThP 005 **Beyond Edman Degradation: Automated** *de novo* **Protein Sequencing of Modified Monoclonal Antibodies**; Nuno Bandeira¹; Victoria Pham²; David Arnott²; Jennie Lill²; Pavel Pevzner³; ¹Center for Computational Mass Spectrometry, UCSD, La Jolla, CA; ²Genentech Inc, South San Francisco, CA; ³University of California, San Diego, La Jolla, CA
- ThP 006 PepNovo+: Extending the Performance Envelope of de novo Sequencing; Ari Frank; Pavel Pevzner; UCSD, La Jolla, CA
- ThP 007 **Lipid Analytical Tool (LipidAT): Automated Analysis of Lipidomic Mass Spectrometry Data**; <u>Jun</u>
 <u>Ma</u>; Haixu Tang; *Indiana University, Bloomington, IN*
- ThP 008 LipiDiff: A Tool for High-Throughput
 Glycerophospholipid Profiling and Quantitative
 Difference Testing via Direct Infusion Electrospray
 Ionization Mass Spectrometry; Peter S. Straub; Eric I.
 Purser; David L. Tabb; Vanderbilt University,
 Nashville, TN
- ThP 009 ICC-CLASS: Isotopically-Coded Cleavable Cross-Linking Analysis Software Suite; Evgeniy Petrotchenko; Christoph Borchers; UVic-GBC Proteomics Centre, Victoria, Canada
- ThP 010 A Database Search Algorithm for Identification of Intact Cross links in Proteins and Peptides Using Tandem Mass Spectrometry; Hua Xu¹; Pang-hung Hsu²; Liwen Zhang³; Michael A. Freitas³; ¹University of Illinois at Chicago, Chicago, IL; ²The Genomics Research Center, Academia Sinica, Taipei, Taiwan; ³Ohio State University, Columbus, OH
- ThP 011 Spectral Clustering for Comprehensive PTM
 Discovery and Targeted Quantitative Proteomics
 Analysis of Human Lens Proteins; Jayson A.
 Falkner¹; Phillip Wilmarth²; Jarret Falkner¹; Larry
 David²; Isingle Organism Software, Beaverton, OR;
 BMB, OHSU, Portland, OR
- ThP 012 Correlation of MS2 and MS3 Pairs for Phosphoprotein Identification; Bret Cooper; USDA-ARS, Beltsville, MD

- ThP 013 Sequencing of Cyclic Non-Ribosomal Peptides Using High Accuracy Mass Spectrometry Data; Julio Ng¹; Nuno Bandeira¹; Wei-ting Liu¹; Roger Linington²; Pieter Dorrestein³; Pavel Pevzner¹; ¹University of California, San Diego, La Jolla, CA; ²University of California, Santa Cruz, Santa Cruz, CA; ³University of California, San Diego, Skaggs School, La Jolla, CA
- ThP 014 BUPID-Top-Down: Database Search and
 Assignment of Top-Down MS/MS Data; Weiwei
 Tong; Roger Theberge; Giuseppe Infusini; Weidong
 Cui; David H. Perlman; Cheng Lin; Mark E. Mccomb;
 Catherine E. Costello; Boston University School of
 Medicine, Boston, MA
- ThP 015 Fast Unrestrictive Identification of Multiply-Modified Peptides; Seungjin Na¹; Nuno Bandeira²; Eunok Paek¹; ¹Univ. of Seoul, Seoul, South Korea; ²Center for Computational Mass Spectrometry, UCSD, La Jolla, CA
- ThP 016 **HeXicon++: Automating HDX Data Analysis**; Xinghua Lou¹; Bernhard Y. Renard¹; Marc Kirchner²; Ullrich Koethe¹; Christian Graf³; Judith A.J. Steen²; Hanno Steen²; Matthias P. Mayer³; Fred Hamprecht¹;

 ¹University of Heidelberg, Heidelberg, Germany;

 ²Children's Hospital Boston / Harvard Medical, Boston, MA; ³ZMBH, Heidelberg, Germany
- ThP 017 HDX by nanoLC-MALDI: Software for Discovery of Protein-Wide Correlations between Peptide Deuterium Uptake Data and Structural or MD Simulation Parameters; Vikram Bodicherla; Paul Gershon; UC-Irvine, Irvine, CA
- ThP 018 Marimba: A Toolset for Automated Design of High-Throughput LC-MRM/MS Assays from Prior Shotgun Proteomics Analyses; Angel D. Pizarro¹; Sumit Shah¹; Kenneth Yu¹; Samuel I. Parry¹; Garret A. FitzGerald²; Ian A. Blair²; ¹University of Pennsylvania, Philadelphia, PA; ²Univ. of Penn/SOM/Pharmacol, Philadelphia, PA
- ThP 019 Automated Creation and Refinement of Complex Scheduled SRM Methods for Targeted Proteomics;

 Brendan Maclean¹; Daniela Tomazela¹; Amol Prakash²; Scott Peterman³; Michael J. Maccoss¹; ¹University of Washington, Seattle, WA; ²ThermoFisher Scientific, Cambridge, MA; ³Thermo Electron, Somerset, NJ
- ThP 020 Statistical Analysis of Calibration Curves on Log-Log Scale from Multiple Reaction Monitoring Assays for Measuring Proteins Spiked into Human **Plasma;** Steven J Skates¹; Terri Addona²; Susan E. Abbatiello²; Birgit Schilling³; D. R. Mani⁴; David M. Bunk⁵; Clifford H. Spiegelman⁶; Lisa Zimmerman⁷; Amy-joan L. Ham⁸; Hasmik Keshishian⁴; Steven C. Hall⁹; Steven A. Carr²; CPTAC Network¹⁰; ¹Massachusetts General Hospital, Boston, MA; ²Broad Institute, Cambridge, MA; ³Buck Institute for Age Research, Novato, CA; ⁴Broad Institute of MIT, Cambridge, MA; ⁵National Institute of Standards and Technology, Gaithersburg, MD; ⁶Texas A&M University, College Station, TX; ⁷Vanderbilt University, Nashville, TN; 8Vanderbilt University School of Medicine, Nashville, TN; 9UCSF MS Core Facility, San Francisco, CA; ¹⁰National Cancer Institute, Bethesda,
- ThP 021 Database Searching of Combined ETD and CID
 Data Using Protein Prospector; Peter R Baker; Robert
 Chalkley; Aenoch Lynn; Shenheng Guan; A.L.
 Burlingame; University of California, San Francisco,
 CA

- ThP 022 Decreasing Database Search Times in ETD MS/MS Sequence Searching by Assignment of Parent Precursor Charge to MS/MS Spectra; Viswanadham Sridhara; Lewis Y. Geer; Stephen H. Bryant; NCBI/NLM/NIH, Bethesda, MD
- ThP 023 Charge Prediction Machine: A Tool for Inferring Precursor Charge States of Electron Transfer Dissociation Tandem Mass Spectra; Paulo C Carvalho^{1,2}; Daniel Cociorva¹; Catherine C L Wong¹; Maria da Gloria da C Carvalho²; Valmir C Barbosa²; John Yates¹; ¹The Scripps Research Institute, La Jolla, CA; ²Federal University of Rio de Janeiro, Rio de Janeiro, Brazil
- ThP 024 Modeling ETD Fragmentation with Bayesian Network for Peptide Identification; Xiaowen Liu¹; Baozhen Shan²; Bin Ma¹; ¹University of Waterloo, Waterloo, Canada; ²Bioinformatics Solutions Inc., Waterloo, ON
- ThP 025 Statistical Discovery and Applications of Fragmentation Patterns from Proteomics-Grade Electron Transfer Dissociation (ETD) Spectra; Ruixiang Sun^{1,2}; Meng-Qiu Dong³; Bing Yang³; Hao Chi^{1,2}; Liyun Xiu^{1,2}; You Li^{1,2}; Wenping Wang^{1,2}; Chao Liu^{1,2}; Leheng Wang^{1,2}; Yan Fu^{1,2}; Si-Min He^{1,2}; Institute of Computing Technology, CAS, Beijing, China; ²Key Lab of Intelligent Information Processing, CAS, Beijing, China; ³National Institute of Biological Sciences, Beijing, China
- ThP 026 Increasing Peptide Identifications Using Spectral Processing Prior to a Database Search; David Good¹; Craig Wenger²; Joshua J. Coon³; ¹Univeristy of Wisconsin, Madison, WI; ²University of Wisconsin, Madison, WI Madison, WI; ³Univ of Wisconsin-Madison, Madison, WI
- ThP 027 MS-Based Proteomics of Oceanic Microbial Communities Using High-Performance Computing, Sequence Similarity, Peptide Coverage Mapping, and Confidence Metrics; Angela D. Norbeck¹; Christopher Oehmen¹; Matthew E. Monroe¹; Carrie D. Nicora¹; Ashoka D. Polpitiya¹; Heather Mottaz-Brewer^{1,4}; Sarah Sowell³; Lea Constan²; Stephen Giovannoni³; Steven Hallam²; Liljiana Paša-Tolić^{1,4}; Mary S. Lipton¹; Richard D. Smith¹; *Pacific Northwest National Laboratory, Richland, WA; *University of British Columbia, Vancouver, Canada; *3Oregon State University, Corvallis, OR; *4Environmental and Molecular Sciences Laboratory, Richland, WA
- ThP 028 Quadrupole Time-of-Flight Mass Spectrometry to Characterize the Proteome of an Unsequenced Genome –Mangifera indica; Pradip Kumar Acharya¹; Keshava T.S. Prasad¹; Harsh A Pawar¹; Sameer Kumar¹; Renu Goel¹; Rajesh Raju¹; Santosh Renuse¹; H C Harsha^{1,2}; Raghothama Chaerkady^{1,2}; Akhilesh Pandey²; Institute of Bioinformatics, Bangalore, India; ²Johns Hopkins University, Baltimore, MD
- ThP 029 Confident Identification of Single Amino Acid Polymorphisms by a Database-Searching Approach for Shotgun Proteomics; Chongle Pan¹; P. Douglas Hyatt¹; Nathan C. Verberkmoes¹; Jill F. Banfield²; Robert Hettich¹; ¹Oak Ridge National Laboratory, Oak Ridge, TN; ²University of California, Berkeley, CA
- ThP 030 An Automated Method for Resolving Gene Sequencing Errors through Tandem Mass Spectrometry; Robert M. Day^{1,2}; Tamah Fridman^{1,2}; Nathan C. Verberkmoes¹; Loren Hauser¹; Doug Hyatt¹; Andrey Gorin¹; ¹Oak Ridge National Laboratory, Oak

- Ridge, TN; ²Joint Institute for Computational Sciences, Oak Ridge, TN
- ThP 031 Investigating Amino Acid Polymorphisms in a
 Natural Viral-Microbial Community by Integrating
 High Mass Accuracy and de novo Search
 Algorithms; Patricia Carey¹; Chongle Pan¹; Manesh
 Shah¹; Robert Hettich¹; Mya Breitbart²; Jillian
 Banfield³; Nathan C. Verberkmoes¹; Ioak Ridge
 National Lab, Oak Ridge, TN; University of South
 Florida, St. Petersberg, FL; University of California,
 Berkeley, Berkeley, CA
- ThP 032 Withdrawn

PROTEOMICS: BIOMARKER DISCOVERY, 033 - 064

- ThP 033 Effect of Preimplantation Factor (PIF)* on Autoimmune Neuroinflammation (Multiple Sclerosis) Using Discovery Proteomics; Ravi
 Amunugama¹; Michael Ford¹; Richard Jones¹; Lola Weiss²; Reuven Or²; Sivakumar Ramu^{3,4}; Zhanna Yachtin²; Eytan Barnea^{3,5}; ¹NextGen Sciences, Ann Arbor, MI; ²Hebrew University, Jerusalem, Israel; ³BioIncept LLC, Cherry Hill, NJ; ⁴Cari Reproductive Institute, Chicago, IL; ⁵Society for the Investigation of Early Pregnancy, Cherry Hill, NJ
- ThP 034 Classification of MALDI-TOF Profile Spectra of Spinal Cord Tissue from Control and ALS Patients;

 Joshua L. Johnson¹; Long Li¹; Daryl A. Bosco²; Robert H. Brown Jr²; Pengyu Hong¹; Jeffrey N. Agar¹;

 Brandeis University, Waltham, MA; ²University of Massachusetts Medical School, Worcester, MA
- ThP 035 Using Cell Fractionation and Metabolic Labeling to Identify Serum Biomarkers of Liver Damage; Julie A Weisz¹; Hidekazu Tsukamoto²; Christine C Wu³;

 **IUniversity of Colorado School of Medicine, Aurora, CO; ²UCLA, Los Angeles, CA; ³University of Colorado, Aurora, CO
- ThP 036 Identification of Brugia Worm Proteins by Life Cycle Stage; Tiffany Weinkopff^{1,2}; Xiang Zhu¹; Rohan Patel¹; John John¹; William Jones¹; Patrick Lammie²; Ron Orlando¹; **Iuniversity of Georgia, Athens, GA; **2CDC, Atlanta, GA**
- ThP 037 Biomarker Candidate Discovery from Formalin-Fixed and Paraffin-Embedded Tissue Microarrays: Combining Electrophoresis and MALDI FT-ICR MS; Hans-Rudolf Aerni; Dale S. Cornett; Richard M. Caprioli; Vanderbilt University, Nashville, TN
- ThP 038 Differential Gel Electrophoresis of Bovine Samples
 Treated with Zeranol to Determine the Mechanism
 of Positive Muscle Growth in Cattle; Jocelyn Hach;
 Young C Lin; Wei-Ping Ye; John Mark Reddish; Kari
 Green-Church; Macdonald Wick; The Ohio State
 University, Columbus, OH
- ThP 039 High Throughput Sample Preparation for Stroke Biomarker Discovery Using the Digital Proteome Chip; David Sarracino²; MingMing Ning¹; Amol Prakash²; Taha Rezai²; Bryan Krastins²; Michael Athanas³; Mary F Lopez²; ¹Massachusettes General Hospital, Boston, MA; ²ThermoFisher Scientific, Cambridge, MA; ³VAST Scientific, Wayland, MA
- ThP 040 Proteomics Analysis of the Human Embryonic Stem Cell Secretome Reveals Novel Differentiation Factor Candidates; Qiangwei Xia; Guokai Chen; James A. Thomson; Joshua J. Coon; Univ of Wisconsin, Madison, Madison WI
- ThP 041 Multiplex iTRAQ-Based Quantitative Approach for Cochlear Nucleus Proteomics in a Mouse Model of Age-Related Hearing Loss (AHL); Harsha P.

- <u>Gunawardena</u>; Ling Xie; Yanbao Yu; Heather O'Donohue; Paul B. Manis; Xian Chen; *University of North Carolina, Chapel Hill, NC*
- ThP 042 Glycan Biomarker Discovery of Adult Stem Cells
 Using Sequential Mass Spectrometry; Jenny Jiao¹;
 Hailong Zhang¹; Krisha Panchalingam²; James L.
 Sherley²; Vernon N. Reinhold¹; ¹The Glycomics Center,
 University of New Hampshire, Durham, NH 03824;
 ²Boston Biomedical Research Institute, Watertown, MA
- ThP 043 Leveraging MS/MS Spectra for Optimizing SRM
 Transitions for Hypothesis-Driven Biomarker
 Discovery in Human Plasma; Simon Letarte¹; Miyoun Brusniak³; Jungchun Chen³; Hamid Mirzaei¹;
 Emma Nimeus²; Carey Sheu¹; Julian D Watts¹; Ruedi Aebersold^{1,3}; Institute for Systems Biology, Seattle, WA; ²University Hospital, Lund, Sweden; ³Swiss Federal Institute of Technology, Zurich, Switzerland
- ThP 044 ER Stress Pathway Related Prostate Cancer
 Biomarker Discovery from Needle Core Biopsy
 Samples Following Step-Wise Density Based
 Extraction and MALDI-TOF/TOF; Wendy Lan;
 Marc Horn; Prospect Biosystems, Inc., Newark, NJ
- ThP 045 Profiling the Prostate Cancer Plasma Membrane N-Glycoproteome via a Highly Specific Glycopeptide-Capture Chemistry; Amelia C. Peterson¹; Priti Koranne²; Bernd Wollscheid³; Daniel B. Martin²;

 ¹University of Wisconsin-Madison, Madison, WI;

 ²Institute for Systems Biology, Seattle, WA; ³IMSB, ETH Zurich, Zurich, Switzerland
- ThP 046 Label-Free Quantitative Analysis of Glycoproteins Enriched through Lectin Affinity Chromatography of Human Serum: Application to the Study of Esophageal Adenocarcinoma; Benjamin Mann¹; Milan Madera²; Yehia Mechref²³³; Milos V. Novotny¹¹²; Indiana University, Bloomington, IN; ²National Center for Glycomics and Glycoproteomics, Bloomington, IN; ³METACyt Biochemical Analysis Center, Bloomington, IN
- ThP 047 A SILAC Study of Neurofibromatosis: Evaluating the Proteome of Tumor Specimen and Nf1-/-Primary Cells; Douglas A Johnson¹; Catherine Formolo^{1,2}; Tobey MacDonald¹; Karlyne Reilly³; Roger Packer¹; Yetrib Hathout^{1,2}; ¹Children's National Medical Center, Washington, DC; ²George Washington University, Washington, DC; ³National Cancer Institute, Frederick, MD
- ThP 048 Application of a Rationally Designed Gas Phase
 Fractionation Technique to Isotope Coded Affinity
 Tagging; Kristian E. Swearingen; Martin Sadilek; Brad
 T. Cookson; Norman J. Dovichi; University of
 Washington, Seattle, WA
- ThP 049 Enrichment and Identification of Low Abundance Proteins Using Hexapeptide Libaries; Martha Stapels²; Catalin Doneanu²; Kate Smith¹; Weibin Chen²; ¹Bio-Rad Laboratories, Hercules, CA; ²Waters Corporation, Milford, MA
- ThP 050 Improved Proteomic Approach for the Discovery of Potential Vaccine Targets in Trypanosoma Cruzi;

 Ernesto S. Nakayaasu¹; Tiago J.P. Sobreira²; Rafael
 Torres Jr.¹; Luciane Ganiko¹; Paulo S.L. Oliveira²;
 Alexandre F. Marques¹; Igor C. Almeida¹; ¹University
 of Texas at El Paso, El Paso, TX; ²Instituto do
 Coracao, Universidade de Sao Paulo, Sao Paulo,
 Brazil
- ThP 051 Comprehensive Plasma Analysis for Finding Pathogenic Factors in Preeclampsia; Chongdong

- Liu²; <u>Haiqiang Yu¹</u>; Yong Liang¹; Yang Xu²; Haiteng Deng¹; Zhenyu Zhang²; ¹The Rockefeller University, New York, NY; ²Beijing Chaoyang Hospital affiliated Capital Medic, Beijing, China
- ThP 052 LC-MS Analysis of Proteins Secreted By Activated Pancreatic Stellate Cells; Angela Y Wehr¹; Kenneth Yu¹; Ian A. Blair²; ¹University of Pennsylvania, Philadelphia, PA; ²Univ. of Penn/SOM/Pharmacol, Philadelphia, PA
- ThP 053 Identification and Quantitation of Plasmodium falciparum and Anopheles gambiae Proteins from Plasmodium Parasite Infected Mosquitoes Using Isotope Labeling; Raghothama Chaerkady^{1,2}; Mobolaji A Okulate¹; Kumaran Kandasamy^{1,2}; Sutopa B Dwivedi²; Nirbhay Kumar¹; Akhilesh Pandey¹; ¹Johns Hopkins University, Baltimore, MD; ²Institute of Bioinformatics, Bangalore, India
- ThP 054 Relative Quantification in Mass Spectrometry Based Proteomics Studies: Understanding Bias and Variability in an iTRAQ Spike-in Study; Ann L Oberg¹; Douglas Mahoney¹; Carrie Holtz-heppelmann¹; Linda M Benson¹; Leeann Higgins²; Terry Therneau¹; Gary Nelsestuen²; H. Robert Bergen, III¹; ¹Mayo Clinic, Rochester, MN; ²University of Minnesota, Minneapolis, MN
- ThP 055 SILAC Based Quantitative Proteomics Approach to Identify Secreted Biomarkers of Esophageal Squamous Cell Carcinoma; Manoj K. Kashyap^{1,2}; H. C. Harsha^{1,2}; Santosh S. Renuse²; Harsh A. Pawar²; Min-Sik Kim¹; Arivusudar Marimuthu^{1,2}; Raghothama Chaerkady^{1,2}; Anil K. Rustgi³; Akhilesh Pandey¹;

 ¹Johns Hopkins University, Baltimore, MD; ²Institute of Bioinformatics, Bangalore, India; ³University of Pennsylvania, Philadelphia, Pennsylvania
- ThP 056 A Quantitative Label-Free Profiling Study of the Effects of Hypoxia on Mycobacterium Tuberculosis Membrane and Cytosol Proteins; Hua Lin; Jing Wang; Thomas A. Shaler; Chris Becker; PPD Biomarker Discovery Sciences, Menlo Park, CA
- ThP 057 Identification of Potential Biomarkers of Esophageal Squamous Cell Carcinoma Using Quantitative Proteomics; Santosh Renuse²; Pradip Kumar Acharya²; H.C. Harsha^{1,2}; Nandini Patankar²; Manoj K Kashyap^{1,2}; Yashwanth Subbannayya²; Harsh Pawar²; Raghothama Chaerkady^{1,2}; Rekha V Kumar³; Akhilesh Pandey¹; ¹Johns Hopkins University, Baltimore, MD; ²Institute of Bioinformatics,, Bangalore, India; ³Kidwai Memorial Institute of Oncology, Bangalore, India
- ThP 058 Comparative Proteomic Profiling of Osteoarthritis and Rheumatoid Arthritis; Nandini Patankar¹; Mitali Bhattacharjee¹; Harsh Pawar¹; Charles Jacob Harrys Kishore¹; H. C. Harsha^{1,2}; Santosh Renuse¹; Raghothama Chaerkady^{1,2}; Shankar Subramanian³; Akhilesh Pandey²; Institute of Bioinformatics, Bangalore, India; Johns Hopkins University School of Medicine, Baltimore, MD; Armed Forces Medical College, Pune, India
- ThP 059 Identification of Secreted Biomarkers of Pancreatic Cancer Using SILAC; H.C. Harsha^{1,2}; Jun Zhong¹; Arivusudar Marimuthu^{1,2}; Manoj K Kashyap^{1,2}; Sameer Kumar²; Raghothama Chaerkady^{1,2}; <u>Akhilesh Pandey</u>¹; If Johns Hopkins University, Baltimore, MD; Institute of Bioinformatics, Bangalore, India
- ThP 060 Evaluation of Formalin Fixed Paraffin Embedded Tissues for the Extraction and Comparison of Peptide Phosphorylation; Paul L Auger Jr²;

- Christopher Farnsworth³; Kimberly Lee²; Leo E. Bonilla²; Mike Davis¹; ¹Amgen, Inc., Thousand Oaks, CA; ²Amgen, Thousand Oaks, CA; ³Molecular Sciences-Amgen, Seattle, WA
- ThP 061 Identification of Differentially Modified Proteins in the Astrocytoma Secretome; Catherine Formolo^{1,2}; Kristy J. Brown¹; Tobey J. MacDonald^{1,2}; Yetrib Hathout^{1,2}; ¹Children's National Medical Center, Washington, DC; ²George Washington University, Washington, DC
- ThP 062 Quantitative Neuroblastoma Cell Line Comparison Using a Pooled SILAC Reference Sample; Charlene Bierl; Lin-sheng Li; Logan J Everett; Stephen R Master; University of Pennsylvania, Philadelphia, PA
- ThP 063 Multiplexed On-Target Protein Fractionation for MALDI Analysis of Sub-Proteome "Windows" into Complex Samples; Rachel L Weller Roska; Stephen A Brose; Robert E Carlson; Receptors LLC, Chaska, MN
- ThP 064 Identification of Serum Biomarker in Cysticercossis, the Major Parasitic Disease of the Central Nervous System; Brian J. Ward; Momar Ndao; Christine Straccini; Bernard F. Gibbs; McGill University, Montreal, QC

METABOLOMICS, 065 - 100

- ThP 065 Global Metabolic Profiling in Plasma Samples of Patients Before and After Ketogenic Diet Therapy by Monolithic-C18 LC and HILIC/(+)ESI-MS; Soledad Cerutti; Peggy R. Borum; Jodie V. Johnson; Richard A. Yost; David H. Powell; University of Florida, Gainesville, FL
- ThP 066 Evaluation of Exact Mass and Relative Isotopic Abundance Measurements in LTQ-Orbitrap Mass Spectrometer for Further Metabolomics Database Building; Ying Xu¹; Geoffrey Madalinski¹; Aurelie Roux¹; jean-francois Heilier^{1,2}; Jerome Cotton¹; Eric Ezan¹; Jean-claude Tabet³; Christophe Junot¹; ¹CEA, Gif-sur-Yvette, France; ²Université catholique de Louvain, Bruxelles, Belgique; ³University Paris VI (UPMC), Paris, France
- ThP 067 Determining the Molecular Substrate Specificity of Kidney Anion Transporters in vivo Using Untargeted Metabolomics; William Wikoff¹; Sanjay Nigam³; Gary Siuzdak²; ¹The Scripps Research Intitute, San Diego, CA; ²The Scripps Research Institute, La Jolla, CA; ³University of California San Diego, La Jolla. CA
- ThP 068 Measurement of the Metabolome of Stagonospora Nodorum, a Major Pathogen on Wheat; Robert Trengove 1,3; Joel Gummer 1,2; Kar-Chun Tan 1,2; Peter S Solomon 2,4; Richard P. Oliver 1,2; Murdoch University, Murdoch, Australia; ACNFP, Murdoch, Australia; Metabolomics Australia (Murdoch Node), Murdoch, Australia; Australia National University, Canberra, Australia
- ThP 069 Proof-of-Principle for Untargeted Plasma
 Metabolite Profiling to Discover Metabolic
 Aberrations Resulting from Gene Defects and Drug
 Treatments; Qiuying Chen¹; HC Park²; Brian Ratliff²;
 Michael Goligorsky²; Steven M. Fischer³; Steven S.
 Gross¹; ¹Weill Medical College of Cornell University,
 New York, NY; ²New York Medical College, New York,
 NY; ³Agilent Technologies, Santa Clara, CA
- ThP 070 Combining Unbiased Metabolic Profiling with Targeted Analysis of Specific Metabolites Using High Resolution Mass Spectrometry, a Step Forward in Metabolomics; Albert Koulman¹; Martin

- Hornshaw²; Gary Woffendin²; Helen Welchman²; Vinod Narayana¹; Catharina Crone²; Dietrich Volmer¹; ¹Medical Research Council, Cambridge, UK; ²Thermo Fisher Scientific, Hemel Hempstead, UK
- ThP 071 Mass-Based Global Metabolomics in a Neuropathic Rat Model Implicates the Central Nervous System as the Basis for Chronic Pain; Gary J Patti¹; Oscar Yanes¹; James Bilsland²; Jean-Philippe Courade²; Gary Siuzdak¹; ¹The Scripps Research Institute, La Jolla, CA; ²Pfizer, Pain, Sandwich, UK
- ThP 072 Cuticular Wax Profiling of Individual Arabidopsis Flowers: Use of LVI-PTV-GCMS as a Means of Validating Metabolite Imaging Data; Zhihong Song 1,2; Ji Hyun Jun 1,2; Zhenjiu Liu 1,2; Edward S. Yeung 1,2; Young Jin Lee 1,2; Basil J. Nikolau 1,2; I Ames Lab of US DOE, Ames, IA; I lowa State University, Ames, IA
- ThP 073 Visualization of Identified and Unknown
 Compounds in Metabolomic Data Sets of
 Environmental Tobacco Smoke Exposure in Rats;
 Dinesh Kumar Barupal; Oliver Fiehn; UC Davis, Davis,
 C4
- ThP 074 Optimization of Cell-based Protein Production
 Using Quantitative Targeted Metabolite Analysis of
 Animal Cell Cultures; Denise U. Sonntag; Michael
 Urban; Matthias Keller; Klaus M. Weinberger;
 Biocrates Life Sciences AG, Innsbruck, Austria
- ThP 075 An Automated Processing Pipeline for Accurate

 Mass LC-MS Data Enabling Combined

 Identification and Quantitation of Metabolites; Ryan

 M. Danell¹; Jun Han²; Christoph Borchers²; ¹Danell

 Consulting, Greenville, NC; ²UVic-GBC Proteomics

 Centre, Victoria, BC
- ThP 076 Ultra-Fast Quantitative Profiling of Endogenous Metabolites Based on Differential Chemical Labelling and MALDI-MS; Dietrich A Volmer; Daniel Petras; Vinod Narayana; Albert Koulman; Medical Research Council, Cambridge, UK
- ThP 077 Mass Spectrometry Based Metabonomics Study on Autism; Jun Yang, Jozsef Lango; Bruce D. Hammock; University of California, Davis, Davis, CA
- ThP 078 Metabolomics Reveals Unique Medicago truncatula Responses to the Devastating Phymatotrichopsis Root Rot Pathogen and Strategies for Metabolic Engineering of Resistance; Wensheng Li^{1,2}; Guoan Shen¹; Srinivasa Rao Uppalapati¹; Kirankumar S. Mysore¹; Richard A. Dixon¹; Lloyd W. Sumner¹; ¹The Noble Foundation, Ardmore, OK; ²Monsanto, Inc., St. Loyis MO.
- ThP 079 **Human Metabotypes Associate with Genotypes and** Environmental Challenge; Rui Wang-Sattler¹; Christian Gieger¹; Yao Yu²; Kirstin Mittelstrass¹; Eva Lattka¹; Elisabeth Altmeier¹; Karl H Ladwig¹; Norbert Dahmen³; Pei Hao²; Yixue Li²; Lei Liu²; Ludwig Geistlinger¹; Martin Hrabe de Angelis^{1,4}; Florian Kronenberg⁵; Thomas Meitinger^{1,6}; Hans-Werner Mewes^{1,4}; H.-Erich Wichmann^{1,6}; Klaus M. Weinberger⁷; <u>Jerzy Adamski</u>^{1,4}; Karsten Suhre^{1,6}: Thomas Illig^{1,6}; ¹Helmholtz Zentrum Muenchen, Neuherberg, Germany; ²Chinese Academy of Sciences, Shanghai, China; ³University of Mainz, Mainz, Germany; ⁴Technische Universitaet Muenchen, Munich, Germany; ⁵Innsbruck Medical University, Innsbruck, Austria; ⁶Ludwig Maximilian Universitaet, Munich, Germany; ⁷Biocrates Life Sciences, Innsbruck, Austria

- ThP 080 Direct Mass Spectrometric Detection of Metabolic Changes in Live Cells: Uninfected vs HTLV-1 Infected T Cells; Prabhakar Sripadi¹; Rebecca L. Easley²; Fatah Kashanchi²; Akos Vertes¹; I George Washington University, Washington, DC; 2 George Washington University School of Medicine, Washington, DC
- ThP 081 Genetic Basis of Metabolome Variation in Yeast; J. Scott Breunig¹; Eugene Melamud¹; Erin N. Smith²; Leonid Kruglyak¹; Joshua Rabinowitz¹; ¹Princeton University, Princeton, NJ; ²The Scripps Research Institute, La Jolla, CA
- ThP 082 Multiplexed Collision Induced Dissociation-LC/TOF MS for Non-target Metabolite Discovery and Profiling; Feng Shi; Chao Li; A.Daniel Jones; Michigan State University, East Lansing, MI
- ThP 083 Influence of Gut Microbiotal Suppression and Recolonization on Host Metabolism: An Integrated UPLC-MS Based Metabonomic and Metagenomic Approach; Jonathan R Swann¹; Elizabeth J Want¹; Kieran M Tuohy²; Glenn R Gibson²; Ian D Wilson³; James Sidaway³; Jeremy K Nicholson¹; Elaine H Holmes¹; Imperial College, London, UK; ²University of Reading, Reading, UK; ³AstraZeneca, Macclesfield, UK
- ThP 084 Investigating the Health of Whale Sharks at the Georgia Aquarium by Direct Analysis in Real Time Metabolic Serum Fingerprinting; Manshui Zhou¹; Alistair D.M. Dove²; David H. Webb²; Julia Kubanek¹; Facundo Fernandez¹; ¹Georgia Institute of Technology, Atlanta, GA; ²Georgia Aquarium Inc, Atlanta, GA
- ThP 085 Sterol Profiling of Phytosterolemia by Ultrahigh Pressure Liquid Chromatography-Mass Spectrometry; Chiun-gung Juo¹; Cheng-long Wang²; Dou-ming Niu³; Ming-shi Shiao⁴; ¹MMRC, Chang Gung University, Tao-yuan, Taiwan; ²GIBMS,, Chang Gung University, Tao-yuan, Taiwan; ³Pediatrics, Taipei Veterans General Hospital, Taipei, Taiwan; ⁴LS, Chang Gung University, Tao-yuan, Taiwan
- ThP 086 LC-FTMS- and NMR-Based Metabolomics Reveal Age-Related Differences in Mice and Humans;

 Quinlyn A. Soltow; Jennifer M. Johnson; Youngja Park; Tianwei Yu; Frederick H. Strobel; Dean P. Jones; Emory University, Atlanta, GA
- ThP 087 Metabolomics Characterization of Metabolic Effect of HIF1a; Ru Wei; Guodong Li; Yuxin Wang; Xu Xu; Kurt Eng; Albert B Seymour; Pfizer RTC, Cambridge, MA
- ThP 088 Metabolomics Characterization of Adipocyte Cell Model; Guodong Li; Yumei Lucy Sun; Debra F Nathan; Albert B Seymour; Ru Wei; Pfizer RTC, Cambridge, MA
- ThP 089 Probing the Metabolic Response of Yeast to Nutrient Limitation by LC-MS/MS; Christopher Crutchfield; Viktor Boer; Patrick Bradley; David Botstein; Joshua Rabinowitz; Princeton University, Princeton, NJ
- ThP 090 Metabolite Variations of Genetic Strain Brassica Seeds Analyzed by Infusion FTMS-Based Metabolomics; Jun Han¹; Ryan M. Danell²; Raju Datla³; Christoph Borchers¹; ¹UVic-GBC Proteomics Centre, Victoria, BC; ²Danell Consulting, Greenville, NC; ³NRC Plant Biotechnology Institute, Saskatoon, SK, Canada
- ThP 091 A Non-Targeted Metabolomics Approach to Metabolite Analysis in a Complex Matrix Using a Sensitive, High Speed Mass Spectrometer; Alina

- <u>Dindyal-popescu</u>¹; Nanqun Zhu²; Thomas O'shea²; Jeffrey Miller³; ¹MDS Analytical Technologies, Concord, Canada; ²Genzyme, Waltham, MA; ³Applied Biosystems, Framingham, MA
- ThP 092 A Bioinformatics Platform for Two Dimensional Gas Chromatography Mass Spectrometry-Based Metabolomics; Bing Wang^{1,2}; Aiqin Fang¹; Charles Buck⁴; Mark Libardoni³; John Heim³; Xiang Zhang¹;

 ¹University of Louisville, Louisville, KY; ²Anhui University of Technology, Ma An Shan, China; ³LECO Coporation, St. Joseph, MI; ⁴Purdue University, West Lafayette, IN
- ThP 093 Global Profiling Studies in Tumour Bearing Mouse Models Using High Mass Accuracy MSn Analysis; Lindsay Lai^{1,2}; Ian Wilson²; Robert Wilkinson²; Rajesh Odedra²; Simon Ashton³; Alan Barnes³; Neil Loftus³;

 **Manchester University, Manchester, UK;
 **2AstraZeneca, Alderley Park, UK; **3Shimadzu, Manchester, UK
- ThP 094 Integration of NMR- and MS-Based Metabolic Profiling Techniques for Structural Determination of Marker Metabolites; Satoko Kakoi¹; Tadashi Nemoto²; Katsutoshi Takahashi²; Kazunori Saito³; Eri Sunaga²; Daichi Yukihira¹; Yoshinori Fujimura¹; Daisuke Miura¹; Hiroyuki Wariishi¹; ¹Kyushu university, Fukuoka, Japan; ²National Institute of Advanced Industrial Science, Tsukuba, Japan; ³Bruker Daltonics Japan, Yokohama, Japan
- ThP 095 Optimisation of Metabolite Extraction from Liver Samples for Metabolic Profiling by UPLC-MS;

 Perrine Masson; Jeremy K Nicholson; Elizabeth J Want; Imperial College, London, UK
- ThP 096 Metabolomic Profiling Using Orbitrap Fourrier
 Transform Mass Spectrometry; Ludovic Muller¹;
 Nathalie Priymenko²; Céline Domange²; Alain Paris²;
 Christophe Junot³; Sandra Alves¹; Jean-claude Tabet¹;

 ¹University Paris VI (UPMC), Paris Cedex O5, France;

 ²INRA, Toulouse, France; ³CEA, Gif-sur-Yvette, France
- ThP 097 Metabolite Profiling and Biochemical Characterization of Bovine Milk Utilizing GC-MS and LC-MS/MS; John Lennon; Carolyn Amoretty; Kurt Boudonck; Metabolon, Inc., Durham, NC
- ThP 098 Comprehensive Profiling of Acylcarnitines in Human Urine by UPLC-MS/MS; Azeret Zuniga; Liang Li; University of Alberta, Edmonton, Canada
- ThP 099 Metabonomic Profiling of Human Plasma: The Impact of Sample Handling and Storage; Bethanne Warrack; Janet Caceres-Cortes; Serhiy Hnatyshyn; Mohammed Jemal; Petia Shipkova; Michael Reily; Bristol-Myers Squibb, Princeton, NJ
- ThP 100 Targeted Metabolomics of Sterols and Cholesterol Derivatives in Mammal Samples; Therese Koal; Peter Enoh; Matthias Keller; Hans-Peter Deigner; Klaus M. Weinberger; Biocrates Life Sciences AG, Innsbruck, Austria

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- ThP 102 Improving Protein Identification Efficiency for Comprehensive Proteome Mapping of Escherichia coli by LC-ESI MS/MS; Xiaoxia Ye; Nan Wang; Liang Li; University of Alberta, Edmonton, Canada

- ThP 103 Improved Protein Coverage and Throughput in Proteomics Using On-Line Multiplexed Enzyme Digestions and Targeted MS/MS with a Modified LTQ-FTICR; Daniel Lopez Ferrer¹; Konstantinos Petritis¹; Andrei Liyu¹; Yufeng Shen¹; Benito Canas²; Kim K. Hixson¹; Richard D. Smith¹; Mikhail Belov¹;

 1 PNNL / Battelle Northwest, Richland, WA;
 2 Universidad Complutense de Madrid, Madrid, Spain
- ThP 104 Integration of Top-Down and Bottom-Up
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 Zhixin¹; Errol Robinson¹; Mikhail Belov¹; Lijliana
 Paŝa-Tolić¹; John Fjeldsted²; Leslie Leonard²; Simon J.
 Prosser³; David Schriemer⁴; Darren F. Lewis⁵; Richard
 D. Smith¹; ¹Pacific Northwest National Laboratory,
 Richland, WA; ²Agilent Technologies, Santa Clara, CA;
 ³Advion BioSciences, Inc., Ithaca, NY; ⁴University of
 Calgary, Calgary, AB; ⁵Idex Health & Science Group,
 Oak Harbor, WA
- ThP 105 Profiling the Thiol-Disulfide Complement of Saccharomyces Cerevisiae Using Organomercurial Enrichment and Multi-Dimensional-nanoLC/MS; Mark J. Raftery; Bioanalytical Mass Spectrometry, Sydney, Australia
- ThP 106 2D RP/RP LC/MS as a Fractionation Tool for the Separation of Peptides in Human Ovarian Cancer Cell Extracts; Monika Dzieciatkowska¹; Tony Tegeler²; Jinsam You²; Mu Wang^{1,2}; Indiana University School of Medicine, Indianapolis, IN; ²Monarch Life Sciences, Indianapolis, IN
- ThP 107 Quantitative Evaluation of Enzymatic Activity of Immobilized Trypsin Microreactors for Protein Digestion and Identification; Ying Long; Troy Wood; SUNY at Buffalo, Buffalo, NY
- ThP 108 Toward Tubulin Proteomics: Separation and Identification of Acidic Peptides Using Offline HighpH RP-HPLC Coupled with Low-pH LC-MS/MS;

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- ThP 109 Investigation of the Clostridium Acetobutylicum
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 Connolly¹; Chris Hughes¹; Jim Langridge¹; Kevin
 Collins¹; Keith R Compson¹; Philippe Soucaille²;
 Gwenaelle Bestel-corre²; **IWaters*, Manchester*, UK;
 Metabolic Explorer*, Saint Beauzire*, France
- ThP 110 Design of 1 Meter Long Monolithic nanoLC
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 Remco Swart; Dionex Corporation, Amsterdam,
 Netherlands
- ThP 111 Automated Sample Loading and Desalting within a MudPIT Experiment to Increase Global Proteomic Identifications; Robert Lj Graham¹; John Lloyd²; Sonja Hess¹; ¹Caltech, Pasadena, CA; ²NIH/NIDDK, Germantown. MD
- ThP 112 An Efficient Microfluidic Chip-Based Proteolytic Reactor for Online ESI-MS Analysis; Peter Liuni; Tamanna Rob; Derek J. Wilson; York University, Toronto, Canada
- ThP 113 High-Resolution Peptide Analysis Using Sub-Two Micron Columns; Reno Nguyen; Joyce Wang; Mark

- Jacyno; Scott Anderson; Wendy Luo; Ian Chappell; *Grace Davison, Deerfield, IL*
- ThP 114 Novel Cleavable Probe for Cysteinyl-Peptide
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 Department of Biochemistry, Vanderbilt University,
 Nashville, TN
- ThP 115 Mapping Reagent Space for Fragment Ion Mass
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 Bajrami; Xudong Yao; Chemistry Department,
 University of Connecticut, Storrs, CT
- ThP 116 Expanding Mass Forbidden Zones in Tandem Mass Spectra for Improved Selectivity of Phosphoryl Fragment Ion Detection Using Peptide Esterification; Bekim Bajrami¹; Yu Shi¹; Pascal Lapierre²; Xudong Yao¹; **Chemistry Department, University of Connecticut, Storrs, CT; **2Biotech Center, University of Connecticut, Storrs, CT
- ThP 117 Evaluation of Dansyl-Peptides MS and MS/MS
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 Emmanuelle Demey¹; Iman Haddad¹; Gennaro
 Marino²; Angela Amoresano²; Joelle Vinh¹; ¹ESPCIParisTech, Paris, France; ²University of Naples
 Federico II, Naples, Italy
- ThP 118 Enhancing the Detectability of Cysteine-Containing Peptides in MALDI-Based Proteomics; Jon M.

 Bruno¹; Carol E. Parker²; Nedyalka Dicheva²; Kristina E. Ile³; Mihaela Mocanu²; Vytas A. Bankaitis³; John C. Edwards¹; ¹Department of Medicine, UNC-CH, Chapel Hill, NC; ²UNC-Duke Proteomics Center, UNC-CH, Chapel Hill, NC; ³Cell and Developmental Biology, UNC-CH, Chapel Hill, NC
- ThP 119 Using Deuterium Oxide to Measure Turnover Rates of Plant Proteins; Xiao Yuan Yang; Wen-Ping Chen; Adrian D. Hegeman; William M. Gray; Jerry D. Cohen; University of Minnesota, Saint Paul, MN
- ThP 120 The Potential of Fluorous Labeling as a Novel Tool to Enrich Low Abundance Cysteinyl-Peptides;
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 Boston University School of Medicine, Boston, MA
- ThP 121 Optimization of UPLC and Orbitrap Analyses for Characterization of Single Proteins and Complex Mixtures; Donald S Kirkpatrick; Corey E Bakalarski; Lilian Phu; Daisy Bustos; Jianjun Zhang; David Arnott; Genentech, Inc., South San Francisco, CA
- ThP 122 Proteomic Analysis of a Sinitang Uptake Response in the Bacterium Deinococcus Radiodurans;

 Jingyueh Jeng; Chiashan Weng; Chia Nan University of Pharmacy & Science, Tainan, Taiwan
- ThP 123 A Proteomic Approach to the Sources and Fate of Proteins in the Bering Sea; Eli Moore¹; Brook Nunn²; David R. Goodlett²; H. Rodger Harvey¹; ¹University of Maryland/CES, Solomons, MD; ²University of Washington, Seattle, WA
- ThP 124 High Throughput Global Proteome Profiling of
 Mammalian Tissue Using Hybrid Triple
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 Brigitte Simons¹; Feng Zhong¹; Jason Hoffert²; ¹MDS
 Analytical Technologies, Concord, Canada; ²NHLBI,
 Bethesda, MD
- ThP 125 Mass Spectrometric Proteome Analysis of the Tardigrade Hypsibius Dujardini, a New Model Organism for Aging Research; Birgit Schilling¹; Aaron W. Miller¹; Ronald Beavis²; Robert E. Hughes¹;

- Bradford W. Gibson¹; ¹Buck Institute for Age Research, Novato, CA; ²University of British Columbia, Vancouver, BC
- ThP 126 Exploring the Structural Heterogeneity of the COP9
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 Lan Huang; University of California, Irvine, CA
- ThP 127 Tandem Mass Spectrometry Analysis of Primary Amyloid Disease Patient Tissue Samples Fractionated by Hydrostatic Pressure Cycling; Zhenning Hong; Giuseppe Infusini; Lawreen H. Connors; Martha Skinner; Catherine E. Costello; Boston University School of Medicine, Boston, MA
- ThP 128 Differential Expression of Cellular Proteins in Pancreatic Cancer Cells in Response to Transketolase Inhibitor Oxythiamine Treatment; Hengwei Zhang¹; Rui Cao¹; W. Paul Lee²; Caishu Deng¹; Yingchun Zhao¹; Jing Xiao¹; Qingmei Xie¹; Shu Lim²; Vay Liang Go²; Robert Recker¹; Gary Guishan Xiao¹; **Icreighton University, Omaha, NE; **2Harbor UCLA Medical Center, Torrance, CA**
- ThP 129 A Novel Method for Protein Profiling in Layered Tissues Combining Serial Sectioning of Frozen Tissue with Gel-Free Label-Free Quantitative Proteomics; Nikolai Skiba^{1,2}; Boris Reidel^{1,2}; Will Thompson³; Arthur Moseley^{1,3}; Vadim Arshavsky²;

 Duke University, Durham, NC; ²Duke University Eye Center, Durham, NC; ³Institute for Genome Science and Policy, Durham, NC
- ThP 130 Development and Use of Complex Experimental Proteomics Standards; Andrew T Bauman¹; Roger Higdon¹; Sean Rapson¹; Brent Louie¹; Jared C. Roach¹; Natali Kolker¹; Gerald van Belle²; Eugene Kolker¹;

 **Seattle Children's Research Institute, Seattle, WA;

 **University of Washington, Seattle, WA

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- ThP 132 Confirmation of Azaspiracid Toxins in Outbreak Implicated Mussel Products; Ann Abraham; Steven M. Plakas; Hudson R. Granade; Kathleen R. El Said; Robert W. Dickey; FDA, Dauphin Island, AL
- ThP 133 Determination of Biogenic Amines in Seafood by GC- and LC-MS; F. Aladar Benesath; Ann Abraham; FDA, Gulf Coast Seafood Laboratory, Dauphin Island, AL
- ThP 134 High Throughput Pesticides Screening Using LC/TOF-MS; <u>Takashi Ando</u>¹; Makiko Iki²; Haruo Hosoda³; Jun Watanabe³; ¹Miyazaki Agricultural Research Institute, Miyazaki, Japan; ²JA Miyazaki Keizairen, Miyazaki, Japan; ³Bruker Daltonics K. K., Yokohama, Japan
- ThP 135 Mass-Spectrometric Analysis of Non-Nitrogen
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 Lapko; Richard Olsen; Lee Zhu; Curtis Sheldon; Chad
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- ThP 136 Analysis of Underivatized Amino Acids in Root Exudates Using Hydrophilic Interaction Liquid Chromatography Combined with Electrospray Ionization Mass Spectrometry; Madeleine Dellmour;

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- ThP 138 Formation Mechanism of Germanium Containing Zeolitic Materials Studied by ESI-MS and ESI-MS/MS; Bernd Bastian Schaack; Ferdi Schueth; Wolfgang Schrader; Max-Planck Inst Coal Res., Mülheim / Ruhr, Germany
- ThP 139 Laser Desorption Ionization on Nanowell Silicon
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 Kececi^{1,2}; Dooho Park^{1,2}; Charles R Martin^{1,2}; Weihong
 Tan^{1,2}; David H Powell^{1,3}; ¹University of Florida
 Department of Chemistry, Gainesville, FL; ²Center for
 Research at Bio/Nano Interface, Gainesville, FL; ³UF
 Metabolomics Core, Gainesville, FL
- ThP 140 Ultra Specific Determination of Clopidogrel in Human Plasma: Improved Method Minimizing Metabolite Back-Conversion; Guy Havard; Marie-Eve Coulombe; Sylvain Lachance; Ann Levesque; Robert Masse; Anapharm, Québec, Canada
- ThP 141 Characterization of DNA Adducts and Secondary Plant Metabolites at the Microgram Level Using a Nanoelectrospray LC-MS-Microcoil NMR Integrated System; Rose Gathungu; Susan Schiavo; John Oldham; Carolyn Lee-Parsons; Paul Vouros; Roger Kautz; Northeastern University, Boston, MA
- ThP 142 Analysis of Canine Kidney Stones Using Mass Spectrometry; James A. Campbell¹; <u>Catherine E. Petersen</u>¹; David S. Wunschel¹; Thomas O. Metz¹; David W. Koppenaal¹; Leo Romanczyk²; Peter Markhill²; John Hammerstone²; <u>Battelle-PNNL</u>, <u>Richland</u>, <u>WA</u>; <u>Waltham</u>, a Division of Mars Incorporated, Leicestershire, UK
- ThP 143 Screening Phosphatidylcholine Injection Samples for Impurities by HPLC-UV-MS and GC/MS; Jamie D. Dunn¹; Jeffrey T. Woodruff¹; John C. Reepmeyer¹; Benjamin J. Westenberger¹; Samia M. Nasr²; Michael E. Hadwiger¹; ¹FDA, CDER, Division of Pharmaceutical Analysis, St. Louis, MO; ²FDA, CDER, Office of Compliance, Silver Spring, MD
- ThP 144 Quality by Design Approach for the Identification of Extractable Substances in Vial Stoppers Using GC/MS and LC/MS for Qualitative Identification; Louis-philippe Labranche¹; John Mchugh³; Yves G. Leblanc¹; Alain Carrier²; Sandoz, Boucherville, Canada; Sandoz Canada, Boucherville, QC; Sandoz Canada, Inc., Boucherville, QC
- ThP 145 **Development of an LC-MS-MS Assay for Cyclooxygenase Inhibition**; <u>Hongmei Cao</u>^{1,2}; Rui

 Yu^{1,2}; Yi Tao^{1,2}; Dejan Nikolic^{1,2}; Richard B. Van

 Breemen^{1,2}; ¹University of Illinois at Chicago, Chicago,

 IL; ²College of Pharmacy, Chicago, IL
- ThP 146 Lipemic Effect Evaluation on Detection Variability
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 Four LC/MS/MS Methods; Nancy Lampron; Sylvain
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- ThP 147 Thermal Gravimetric Analysis Mass Spectrometry (TGA-MS) in the Pharmaceutical Development Setting: Complementing Solid State

- Characterization; John Caesar; Sneha Arekar; Yuegang Zhang; Mariusz Krawiec; Mick Hurrey; Adam Looker; Steve Johnston; Vertex Pharmaceuticals, Cambridge, MA
- ThP 148 Quantitation of Propylene Glycol in Human Plasma by LC/MS/MS: A Bioanalytical Challenge; Serge

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- ThP 149 A LC-MS/MS Method for Quantification of Anthocyanins, Application in a Clinical Pharmacologic Study with a Bioadhesive Black Raspberry Gel Formulation; Yonghua Ling¹; Chen Ren¹; Susan Mallery²; Carlos M. Ugalde²; U.V.R. Vijaya Saradhi¹; Ping Pei²; Gary Stoner^{3,4}; Kenneth K. Chan^{3,5}; Zhongfa Liu^{1,3}; ¹College of Pharmacy, The Ohio State University, Columbus, OH; ²College of Dentistry, The Ohio State University, Columbus, OH; ³Comprehensive Cancer Center, The Ohio State University, Columbus, OH; ⁴College of Medicine, The Ohio State University, Columbus, OH; ⁵Colleges of Pharmacy & Medicine and Public Health, Columbus, OH
- ThP 150 A Novel Method for the Determination of Oxalic Acid in Root Exudates; Leonhard Jaitz; Bernhard Müller; Madeleine Dell'mour; Eva Oburger; Markus Puschenreiter; Gunda Koellensperger; Stephan Hann; University of Natural Resources and Applied Life S, Vienna, Austria
- ThP 151 Evaluation of Two Innovative Derivatization
 Reagents: Application to the Determination of
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 Plasma by LC/MS/MS; Guy Havard; Serge Auger;
 Sylvain Lachance; Johanne Lefebvre; Ann Levesque;
 Robert Masse; Anapharm, Ouébec, Canada
- ThP 152 High Resolution Mass Spectrometry Analysis of 2-Substituted Benzothiazoles; <u>Jian Guo</u>; Scott W. Grimm; *AstraZeneca Pharmaceuticals, Wilmington, DE*
- ThP 153 Troubleshooting Cross-well Contamination in a 96-Well Plate of Volatile Pharmaceutical Compounds (Methylphenidate and Rivastigmine) during Evaporation Step Using LC/MS/MS; <u>Danielle</u> Bouchard; Philippe Bélanger; Patrice Arcand; Robert Massé; *Anapharm, Quebec, QC*
- ThP 154 Fast Method Development Approach for Multi-Analyte SPE Screening and the Analysis of 6 Different Compounds in Human Plasma by LC/MS/MS; Philippe Belanger; Danielle Bouchard; Patrice Arcand; Robert Massé; Anapharm, Québec, Canada
- ThP 155 Light Exposure of 4-oxo-13-cis-retinoic Acid and 4-oxo-all-trans-Retinoic Acid and Qualitative Analysis of their Degradation by-products Using LC/MS/MS; Sébastien Gagné; Nadine Boudreau; Adrien Musuku; Robert Masse; Anapharm, Quebec, QC
- ThP 156 Mass Spectrometry Based Assay for the Enzymatic Hydrolysis of Pseudo-Prochiral Malonate Diesters;

 Dale A. Rosado, Jr; Thomas Maestri; Douglas Masterson*; University of Southern Mississippi, Hattiesburg, MS
- ThP 157 High-Throughput Screening of Cardiovascular Drugs from Clinical Samples by MALDI MS;

 Eduardo C. Dias; Joey C. Latham; Dan M. Roden;

 Nancy J. Brown; Richard M. Caprioli; Vanderbilt Univ Sch of Med, Nashville, TN
- ThP 158 Alteration of Selective Neurotransmitters in Fetal Brains of Alcohol-Treated Prenatally C57BL/6 mice:

- Quantitative Analysis Using Liquid Chromatography/Tandem Mass Spectrometry Methods; Loubna A. Hammad²; Youssef Sari¹; Marwa M. Saleh²; <u>Yehia Mechref²</u>; ¹Department of Psychology, Indiana University, Bloomington, IN; ²Department of Chemistry, Indiana University, Bloomington, IN
- ThP 159 Matrix-Ionization Laser Desorption (MILD) for Structural Elucidation of Small Molecules; Asanka S Rathnayake¹; Sadish Karunaweera¹; Thushani N. Herath¹; Ellen D. Inutan¹; Charles N. Mcewen²; J Michael Walker³; Sarah Trimpin¹; ¹Wayne State University, Detroit, MI; ²Univ. of the Sciences in PA, Philadelphia, PA; ³Indiana University, Bloomington, IN
- ThP 160 How Low Can We Go? An Evaluation of Strategies for Small-Molecule Analysis by MALDI; Christopher C. Lai; Lawrence R. Phillips; Lyndsay L. Smith; James A. Kelley; NCI/NIH, Frederick, MD

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 Ang²; Peiting Zeng²; Maxime Herve²; Laura Via³;
 Clifton E. Barry³; Markus Stoeckli¹; *Novartis Institutes
 for BioMedical Research, Basel, Switzerland; *Novartis
 Institute for Tropical Diseases, Singapore, Singapore;

 *National Institutes of Health, Bethesda, MD
- ThP 162 **Strategies for Drugs Imaging;** Alice M. Delvolvé; Jeremy Post; Shelley N. Jackson; Amina S. Woods; NIH/NIDA/IRP, Baltimore, MD
- ThP 163 Imaging Mass Spectrometry Provides Chemical Makeup of Samples Prepared by Matrix-Assisted Laser Desorption/Ionization Methods; Thushani N.

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- ThP 164 Imaging Melamine in Egg Samples by Surface
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 Ionization Mass Spectrometry; Haiwei Gu^{1,2};
 Shuiping Yang²; Huanwen Chen^{2,3}; Yuling Yang²; Bin
 Hu²; Xie Zhang²; Yufen Zhou²; Lili Zhang³;

 ¹Validation Resources, LLC, Bend, OR; ²East China
 Institute of Technology, Fuzhou, P.R. China; ³Jilin
 University, Changchun, P. R. China
- ThP 165 Quantitatitive Mass Spectrometric Imaging of Endogenous Acetylcarnitine from Piglet Brain Tissue Using Acetyl-d₃-Carnitine as an Internal Standard; <u>David A. Pirman</u>; Peggy R. Borum; Richard A. Yost; *University of Florida, Gainesville, FL*
- ThP 166 Ambient Molecular Imaging of Matrix-Free Plant
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- ThP 167 Direct Analysis of Irinotecan Metabolites by
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 ¹Thermo Fisher Scientific, San Jose, CA; ²Roswell Park
 Cancer Institute, Buffalo, NY
- ThP 168 MALDI Imaging of Pharmaceuticals in Zebrafish for Discovery and Drug Safety Screening; Stacey R.

- Oppenheimer¹; Jiangwei Li²; ¹Pfizer, Groton, CT; ²Iowa State University, Ames, IA
- ThP 169 Mass Spectrometric Imaging of AFEX treated Corn Stover; Zhen Li¹; Paul Bohn²; Jonathan Sweedler¹;

 'University of Illinois, Urbana, IL; 'Notre Dame University, Norte Dame, IN
- The Use of Imaging MALDI to Probe the
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 Alexis Polley³; ¹SAI, LTD., Manchester, UK; ²SAI,
 Manchester, UK; ³SAI Ltd., Manchester, UK
- ThP 171 MALDI MS Imaging of Tumour Lipids in DU145 and HCT116 Tumour Xenografts and the Effects of Vinblastine; Paul J Trim¹; Kelly M Hearne²; Chris Brown²; Andrew McEwen²; Emmanuelle Claude³; Peter S. Marshall⁴; Alessandra P Princivalle¹; Malcolm Clench¹; ¹Sheffield Hallam Uni, UK, Sheffield, UK; ²Quotient Bioresearch Ltd, Rushden, UK; ³Waters Corporation, Manchester, UK; ⁴GlaxoSmithKline, Stevenage, UK
- ThP 172 Imaging of Phospholipids in Formalin Fixed Rat Brain Sections via MALDI-MS; Claire Louise Carter¹; Cameron McLeod¹; Josephine Bunch²; ¹The University of Sheffield, Sheffield, UK; ²University of Birmingham, Birmingham, UK
- ThP 173 MALDI-FTICR Imaging of Phospholipids in Tissue:
 More Peaks but More Images?; Shannon Cornett¹;
 Hans Rudolf Aerni¹; Richard M. Caprioli²; ¹Vanderbilt
 University, Nashville, TN; ²Vanderbilt Univ Sch of
 Med, Nashville, TN
- ThP 174 A Target Amplification Strategy to Detect Enzyme Activity by Imaging MS; Junhai Yang¹; Pierre Chaurand¹; Ned Porter¹; Richard M. Caprioli²;

 ¹Vanderbilt University, Nashville, TN; ²Vanderbilt Univ Sch of Med, Nashville, TN
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- ThP 177 MALDI Imaging of Phospholipids: Validation of Signal Response; Satu Puolitaival¹; Stephen Milne²; H. Alex Brown³; Richard M. Caprioli⁴; ¹Vanderbilt University, Nashville, TN; ²Vanderbilt University Medical Center, Nashville, TN; ³VUMC Cancer Research, Nashville, TN; ⁴Vanderbilt Univ Sch of Med, Nashville, TN
- ThP 178 High Resolution MALDI Imaging of Lipids and Drug Metabolites in Brain Tissue; Sucharita Dutta¹; Shelley N Jackson²; Alice Devolve²; Amina S. Woods²; Thermo Fisher, San Jose, CA; ²NIDA-IRP, NIH, Baltimore, MD
- The 179 The Localization of Lipids Eye Flat-Mounts by Imaging Mass Spectrometry; Timothy Garrett; William W. Dawson; Richard A. Yost; *University of Florida, Gainesville, FL*
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- ¹Johns Hopkins University School of Medicine, Baltimore, MD; ²Institute of Bioinformatics, Bangalore, India
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- ThP 197 Isolation of C-Terminal Peptides by Strong Anion-Exchanger from Proteolytic Digests of Fully Amidated Proteins for Mass Spectrometric Sequencing; Takashi Nakazawa¹; Mariko Nakagawa¹; Hiroki Kuyama³; Eiji Ando²; Osamu Nishimura³; Minoru Yamaguchi²; Susumu Tsunasawa³; ¹Nara Women's University, Nara, Japan; ²Shimadzu Corp, Kyoto, Kyoto; ³Institute for Protein Research, Suita, Osaka
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 **Thermo Fisher Scientific (Bremen) GmbH, Bremen, Germany;
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 ¹Louisiana State University, Baton Rouge, LA;

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- ThP 207 The Role of Increased Resolution and Scan Speed of Ion Traps for Top-Down Proteomics with ETD/PTR; Michael Schubert; Christian Albers; Andreas Brekenfeld; Christoph Gebhardt; Ralf Hartmer; Bruker Daltonik GmbH, Bremen, Germany
- ThP 208 High-Resolution Orbitrap-ETD for Characterization of Intact HDL Proteins; Matthew Mazur; Helene Cardasis; Yi Du; Nathan Yates; Ronald Hendrickson; Merck Research Laboratories, Rahway, NJ
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 ¹Dept. of Chemistry, UVA, Charlottesville, VA; ²Dept.
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 ¹Central Res. Lab. Hitachi, Ltd., Kokubunji, Japan;
 ²Grad. School Adv. Life Sci., Hokkaido Univ., Sapporo,
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- ThP 243 Precise and Large Scale Identification of Core Fucosylated Glycoproteins by Hybrid Linear Trap/FT-ICR Mass Spectrometer; Wei Jia¹; Yan Fu²; Zhuang Lu¹; Haipeng Wang²; Lina Song¹; Huanhuan Han¹; Jinglan Wang¹; Yun Cai¹; Wantao Ying¹; Simin He²; Xiaohong Qian¹; Istate Key Laboratory of Proteomics-BPRC-BIRM, Beijing, China; Institute of Computing Technology, Beijing, China
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- ThP 245 Improving ETD Analysis of N, O-glycopeptides by
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 Cristina Osorio¹; Maria Warren Hines²; Carol E. Parker²; Oscar Alzate³; ¹University of Chapel Hill, Systems-Proteomics Core, Chapel Hill, NC; ²UNC-Duke Proteomics Center, UNC-CH, Chapel Hill, NC; ³Dept. of Cell and Developmental Biology, UNC-CH, Chapel Hill, NC
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- ThP 253 Elucidation of Cell Surface Glycoproteins from Cancer Stem-Like Cells; Jintang He; Yashu Liu; Xiaolei Xie; Xing Fan; David M. Lubman; University of Michigan, Ann Arbor, MI
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- ThP 262 Mapping Phosphoproteome Dynamics in the Cyanobacterium Circadian Cycle Using Direct LC-MS or LC-MS with On-Line Phosphopeptide Enrichment; Bogdan A. Budnik¹; Joseph S. Markson³; Yelena Margolin²; Alexander R. Ivanov²; John Neveu¹; William S. Lane¹; Erin K. O'Shea³; ¹Harvard University FAS MSPRL, Cambridge, MA; ²Harvard University HSPH, Boston, MA; ³Harvard University, Center for Systems Biology, Cambridge, MA
- ThP 263 Automatic Tandem Immobilized Metal Ion Affinity Chromatography for Enhanced Phosphopeptide Enrichment; Yu-Ni Sun^{1,2}; Yi-Ting Wang²; Chia-Feng Tsai²; Yu-Ju Chen²; ^IInstitute of Bioscience and Biotechnology, NTOU, Taipei City, Taiwan; ²Institute of Chemistry, Academia Sinica, Taipei City, Taiwan
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- ThP 266 Enrichment of Phosphopeptides with Cationic Magnetic Nanoparticles for Mass Spectrometric Analysis; Cheng-Tung Chen; Yen-Peng Ho; National Dong Hwa University, Hualien, Taiwan
- ThP 267 TiOx Nanostructured Coating on MALDI Plates for Capture of Phosphopeptides; Paolo Soffientini¹; Andrea Di Fonzo¹; Roberta Carbone²; Simone Vinati²; Gabriela Grigorean³; ¹Cogentech, Milan, Italy; ²Tethis s.r.l, Milan, Italy; ³IFOM-IEO, Milan, Italy
- ThP 268 Identification of Phosphorylation Sites in Caspase-7 by Mass Spectrometry; Xin Cong; Bradford W. Gibson; Lisa Ellerby; Buck Inst. for Age Research, Novato, CA
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- ThP 271 Nanoprobe-Based Immobilized Metal Affinity
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 Konstantin Aizikov¹; Xiaojuan Li¹; Cheng Lin¹; Peter

 B. O'Connor²; **Iboston University School of Medicine, Boston, MA; **2University of Warwick, Coventry, UK
- ThP 273 Characterization of Glyoxal and Methylglyoxal-Induced Modifications in Human Hemoglobin by NanoLC-Nanospray Ionization Tandem Mass Spectrometry; Yu-chin Chen; Hauh-Jyun Candy Chen; National Chung Cheng University, Ming-hsiung, Taiwan
- ThP 274 Mass Spectrometry-Based Characterization of Protein Glutathionylspermidine Modification Using Complementary Dissociation Approaches; Chi-Chi Chou¹; Kuan-Ting Pan¹; Bing-Yu Chiang²; Chun-Hung Lin²; Kay-hooi Khoo¹.²; ¹NRPGM MS Facilities at Academia Sinica, Taipei, Taiwan; ²IBC, Academia Sinica, Taipei, Taiwan
- ThP 275 Glutamine Deamidation: Differentiation of Glutamic Acid and γ-Glutamic Acid in Peptides by Electron Capture Dissociation; Xiaojuan Li¹; Weidong Cui¹; Chunxiang Yao¹; Konstantin Aizikov¹; Tzu-Yung Lin¹; Nadezda P. Sargaeva¹; Cheng Lin¹; Peter B. O'connor²; ¹Boston University School of Medicine, Boston, MA; ²University of Warwick, Coventry, UK
- ThP 276 Improving the Selectivity of Titanium Dioxide-Based Enrichment of Sulfated Peptides; Katie Hersberger; Kristina Hakansson; University of Michigan, Ann Arbor, MI
- ThP 277 SUMOylation of E1: Determination of SAE2
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 Yuan Chen; City of Hope, Duarte, CA
- ThP 278 Substrate Specificity of TPST-1 and -2 Using Gastrin mutants: An MS Approach; Peter J.

 Ludden¹; Lieza Marie Danan²; Julie A. Leary¹;

 Department of Molecular and Cellular Biology, Davis, CA; Department of Chemistry, Davis, CA
- ThP 279 Molecular Recognition Specificity and Bioaffinity
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 Przybylski¹, ¹University of Konstanz, Konstanz,
 Germany; ²Washington University, St. Louis, Missouri

- ThP 280 Identifying Characteristic Neutral Mass Losses and Low Mass Ions for Oxidized Amino Acids; Jessica M. Saladino¹; Joshua S. Sharp²; ¹Univeristy of Georgia, Athens, GA; ²University of Georgia, Athens, GA
- ThP 281 Application of MALDI TOF/TOF CID Tandem
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 Centocor R&D. Radnor, PA
- ThP 282 A Novel Modification in Somatostatin Fragment (7-14) Under Oxidative Stress; Wei Wu; Peiran Liu; Michael Ackerman; Li Tao; Reb Russell; Michael Grace; Bristol Myers Squibb Co., Pennington, NJ
- ThP 283 Analytical Methods for Improving Identification of SUMO-Modified Peptides; Omoruyi Osula²; Steve Swatkoski¹; Robert J. Cotter³; ¹Department of Pharmacology, Baltimore, MD; ²Johns Hopkins University, Baltimore, MD; ³Middle Atlantic MS Laboratory, Baltimore, MD
- ThP 284 Orientation of Lasso Peptide Fragmentations Under CID and ECD Conditions; Severine Zirah¹; Carlos Afonso²; Uwe Linne³; Kok-Phen Yan¹; Thomas A Knappe³; Mohamed A Marahiel³; Sylvie Rebuffat¹; Jean-claude Tabet²; ¹National Museum of Natural History / CNRS, Paris, France; ²University Paris 6, Paris, France; ³Philipps University, Marburg, Germany
- ThP 285 Specific Modification of Citrullinated Peptides
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 University, Ghent, Belgium
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- ThP 287 Sites of Alkylation by Botanical Chemoprevention
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 Evan Small; Richard B. Van Breemen; University of
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- ThP 288 Elucidating Histone PTM Cross-Talk by
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 Peter R Baker; Barbara Panning; Alma L Burlingame;
 UCSF, San Francisco, CA
- ThP 289 Using Mass Spectrometry to Characterize a Novel PTM in the Escherichia Coli Ribosomal Protein S12; Michael Brad Strader¹; Suwako Fujigaki¹; Cai Yun Chen¹; Nina Costantino³; Anthony J. Makusky¹; W. Judson Hervy IV²; Donald L. Court³; Sanford P. Markey¹; Jeffrey A. Kowalak¹; *INIMH/NIH, Bethesda, MD; *2UT-ORNL, Oak Ridge, TN; *3NCI/FCRDC, Fredrick, Maryland
- ThP 290 Histone Isoform Mapping Using Data-Dependent MS/MS of Deutero-Acetylated Tryptic Fragments;
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- ThP 291 Targeted Quantitative Analysis of Acetylated Histone H4 sites K5, K8, K12, K16; Marc Gentzel¹; Asifa Akhtar²; ¹MPI-CBG, Dresden, Germany; ²EMBL, Heidelberg, Germany
- ThP 292 "Bottom-Up" Approaches to Characterizing Novel
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- ThP 293 MS Analysis of Cysteine Modifications Caused by Sample Preparation; Zhouxi Wang; Tomas Rejtar; Zhaohui Zhou; Barry L. Karger; Northeastern University, Boston, MA
- ThP 294 Minimizing Post Translation Modification Artifacts in Biotherapeutic Proteins; Ying-qing Yu; Martin Gilar; John Gebler; Joomi Ahn; Waters Corporation, Milford, MA
- ThP 295 Comprehensive Analysis of the Arabidopsis
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- ThP 296 Analysis of Post-Translationally Modified Peptides
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 ¹Technical Universitiy Munich, Freising, Germany;

 ²Cellzome AG, Heidelberg, Germany; ³Thermo Fisher
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 Chemistry, Göttingen, Germany
- ThP 297 Comparison of ETD-Trap and Q-TOF for Analysis of Post-Translational Modifications; Vaibhav

 Chumbalkar¹; Vadiraja Bhat²; Khatri latha¹; Rebecca Maywald¹; Oliver Bogler¹; ¹UT MD Anderson Cancer Center, Houston, TX; ²Agilent Technologies, Wilmington, DE
- ThP 298 Beyond Monoisotopic Mass: Detection of Peptide PTMs by Isotope Cluster Analysis; Jonathan A Epstein¹; Matthew Olson²; Kenneth Parker³; Peter S. Backlund¹; Marvin Vestal³; Alfred L. Yergey¹; ¹NIH, Bethesda, MD; ²JHMI, Baltimore, MD; ³Virgin Instruments Corp., Sudbury, MA
- ThP 299 High Energy Collision Dissociation of Glycopeptides
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 Zaneer Segu^{1,2}; Yehia Mechref^{1,2}; ¹METACyt
 Biochemical Analysis Center, Bloomington, IN; ²Dept
 of Chemistry, Indiana University, Bloomington, IN
- ThP 300 Advances and Hurdles in O-linked Glycopeptide Analysis; Zsuzsanna Darula²; <u>Katalin F.</u>

 <u>Medzihradszky</u>^{1,2}, ¹UCSF, San Francisco, CA;

 ²Biological Research Center, HAS, Szeged, Hungary
- ThP 301 Free Dinner: Doubling the Numbers of Identified Phosphopeptides by Converting MS3 Spectra into MS2 Mimics; Wiebke A Timm¹; Nurhan Ozlu²; Judith Steen¹; Hanno Steen¹; ¹Harvard Medical School/Children's Hospital Boston, Boston, MA; ²Harvard Medical School, Boston, MA
- ThP 302 Phosphoproteomic Characterization of Insulin Resistance in T2D Using iTRAQ and SIMAC Combined with Multistage Activation and Higher-Energy C-Trap Dissociation MS/MS; Tine E.

 Thingholm; Henning Beck-Nielsen; Michael Gaster; Ole N. Jensen; Univ. of Southern Denmark, Odense, Denmark
- ThP 303 De-Coupling the Identification and Relative Quantitation of Phopshopeptides Using a Real-Time Combination CID and HCD* Using an LTQ-Orbitrap XL; Andrew JK Williamson²; Yvonne Connolly¹; Duncan L Smith¹; ¹Paterson Institute for

- Cancer Research, Manchester, UK; ²SCALPL, University of Manchester, Manchester, UK
- ThP 304 A Chemical Derivatization, Results-Driven Mass Spectrometry Workflow for Sensitive Identification and Relative Quantification of Tyrosine Phosphorylation Sites; John R Griffiths; Anthony D Whetton; University of Manchester, Manchester, United Kingdon
- ThP 305 MS Characterization of Differentially Modified Isoforms of the Homer2 Scaffolding Protein in Brain; Rob Helton²; Karen K Szumlinski¹; Christine C Wu²; ¹University of California Santa Barbara, Santa Barbara, CA; ²University of Colorado School of Medicine, Aurora, CO
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 Copenhagen, Denmark
- ThP 307 Novel Approach to Phosphopeptide Profiling Based on Combination of Liquid Chromatography at Critical Conditions and Mass Spectrometry; Tatiana Yu. Perlova¹; Yelena Margolin⁴; Irina A. Tarasova¹; Anton A. Goloborodko¹; Alexander V. Gorshkov²; Eugene Moskovets³; Alexander R. Ivanov⁴; Mikhail V. Gorshkov¹; Institute of Energy Problems of Chemical Physics, Moscow, Russia; ²N. N. Semenov's Institute of Chemical Physics, Moscow, Russia; ³MassTech Inc., Columbia, MD; ⁴Harvard School of Public Health, Boston. MA
- ThP 308 Selective Enrichment and Quantitative Analysis of the Endogenous Serum Phosphorylated Peptides for Potential Disease Biomarker Discovery; Lianghai Hu¹; Houjiang Zhou¹; Lihai Guo²; Shutao Sun¹; Mingliang Ye¹; Hanfa Zou¹; ¹Dalian Chemical Physics Institute, the CAS, Dalian, Liaoning; ²ASC, Applied Biosystems, Shanghai, China
- ThP 309 Mass Spectrometric Determination of Disulfide Linkages and Glycosylation Sites in Recombinant Therapeutic Proteins Using On-line LC-MS with Electron Transfer Dissociation; Shiaw-lin Wu¹; Zhiqi Hao²; Andreas F Huhmer²; Haitao Jiang¹; William S. Hancock¹; Barry L. Karger¹; Northeastern University, Boston, MA; ²Thermo Fisher Scientific, San Jose, CA
- ThP 310 Evaluation of the Low-Specificity Protease Elastase for the Phosphoproteome Analysis; Bin Wang; Rainer Malik; Erich Nigg; Roman Körner; Max-Planck-Institute of Biochemistry, Munich, Germany

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- ThP 312 Solvent Gradient Used to Vary Ionization Selectivity in Transmission Mode Desorption Electrospray Ionization; Kevin D. Quinn; Troy Wood; University at Buffalo, Buffalo, NY

- ThP 313 Imaging Desorption Electrospray Ionization-Mass Spectrometry and Direct Analysis in Real Time Mass-Spectrometry for the Integral Investigation of Counterfeit Antimalarial Pharmaceuticals; Asiri Galhena; Leonard Nyadong; R. Mitchell Parry; May D Wang; Facundo Fernandez, Georgia Institute of Technology, Atlanta, GA
- ThP 314 Secondary Electrospray Ionization Detection of Explosive Vapors Below 0.02 ppt on a Triple Quadrupole with an Atmospheric Pressure Source; Erica Mesonero²; Juan A. Sillero²; Marta Hernandez³; Juan Fernandez de la Mora¹; ¹Yale University Mechanical Engineering Departmen, New Haven, CT; ²SEADM, Boecillo, Valladolid, Spain; ³CARTIF, Boecillo, Valladolid, Spain
- ThP 315 Analysis of Non-ionic Surfactants on the Surface of Coated Acrylic Paints by Desorption Electrospray Ionization Mass Spectrometry; Chengli Zu; Greg Meyers; Bruce Bell; Melinda Keefe; Dow Chemical Company, Midland, MI
- ThP 316 DART-MS/MS Analysis of Foamed PVC Jar Lids;

 Luke K. Ackerman¹; Gregory O. Noonan¹; Timothy H.

 Begley¹; Catherine Simoneau²; Michele Suman³; ¹USFDA Center for Food Safety, College Park, MD; ²EU

 Comm., Inst. for Health & Consumer Protection, Ispra,
 Italy; ³Barilla G.R. F.Ili SpA, Parma, Italy
- ThP 317 Continuously Monitoring the States of nano-TiO2
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- ThP 318 Transmission-Mode DART TOF MS for the Semi-Quantitative Analysis of Pyrethroid Pesticide-Treated Bednets; Jose J. Perez¹; Michael D. Green²; Christina Y. Hampton¹; Facundo M. Fernandez¹; ¹Georgia Institute of Technology, Atlanta, GA; ²Centers for Disease Control and Prevention, Atlanta, GA
- ThP 319 Preparation and Rapid Analysis of Dry Powders with an Ambient Pressure Desorption Ionization Equipped Mass Spectrometer; Brian D. Musselman; Elizabeth Crawford; Jordan Krechmer; IonSense, Inc., Saugus, MA
- ThP 320 Instant Quality Control of Biodiesel Made from Used Frying Oil by Easy Ambient Sonic-Spray Ionization Mass Spectrometry; Rosana Maria Alberici¹; Vanderlea de Souza²; Gilberto Fernandes de Sá³; Romeu Jose Daroda²; Marcos Nogueira Eberlin¹;

 ¹ThoMSon Mass Spectrometry Laboratory-UNICAMP, Campinas, SP, Brazil; ²National Institute of Metrology-INMETRO, Duque de Caxias, RJ, BRAZIL;

 ³Department of Fundamental Chemistry, UFPE, Recife, PE, Brazil
- ThP 321 **Development of a SPE/DART Assay for Rapid**Narcotics Screening in Urine; Thurman Allsup¹; Brian
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 ¹OpAns, LLC, Durham, NC; ²IonSense, Inc., Saugus,
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- ThP 323 Electrospray-Assisted Laser Desorption Ionization (ELDI) with an Infrared OPO Laser for

- Characterization of Peptides and Proteins; Mark Little¹; Ivory Peng²; Rachel O. Loo²; Eli Margalith¹; Joseph A. Loo²; ¹Opotek, Inc., Carlsbad, CA; ²UCLA, Los Angeles, CA
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 State University, Raleigh, NC
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- ThP 326 Development of a "Greener" Ionization Source for Ambient Desorption Ionization with Nitrogen as the Carrier Gas; <u>Joseph Tice</u>¹; Douglas Simmons²; Michael Festa¹; James A. Hill³; Brian D. Musselman¹; ¹IonSense, Inc., Saugus, MA; ²IonSense Inc., Saugus, MA; ³James A. Hill Instruments, Arlington, MA
- ThP 327 Mass Spectrometry Guided Surgery by Direct Coupling of Electrosurgical Methods with On-line Mass Spectrometric Analysis; Zoltan Takats^{1,2}; Katalin Albrecht¹; Reka Skoumal¹; Miklos Toth¹; Tamas Szaniszlo¹; Karl-Christian Schaefer²; Julia Denes¹; ¹Semmelweis University, Budapest, Hungary; ²Justus-Liebig University, Giessen, Germany
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- ThP 330 Novel Applications of DART (Direct Analysis in Real Time) in Pharmaceutical Industry; Guilong (Charles) Cheng; Pfizer, Inc., Groton, CT
- ThP 331 Off-Line Desorption Electrospray Ionization (Off-Line DESI) for Sample Collection: A Novel Surface Sampling and Preconcentration Technique; Afrand Kamali; Semere Bairu; Shashank Jain; Andre Venter; Western Michigan University, Kalamazoo, MI
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- ThP 335 Atmospheric Pressure Ion Soft Landing and Surface Patterning; Abraham K Badu Tawiah¹; Chunping Wu¹; Hao Chen²; R. Graham Cooks¹; ¹Purdue University, West Layette, IN; ²Ohio University, Athens, OH
- ThP 336 In situ SIMS Analysis and Reactions of Surfaces Prepared by Ion Soft-Landing; Jobin Cyriac; Liang

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- ThP 337 In situ Characterization of Surfaces Following Soft
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 Omar Hadjar³; Julia Laskin¹; ¹Pacific NW National
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 AL
- ThP 338 Characterizaion and Isolation of Specifically Selected Cu Nanoclusters Using Drift Tube Soft Landing; Stephen Davila; Guido F. Verbeck; University of North Texas, Denton, TX
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- ThP 344 Ultra fast Proton-Transfer-Reaction Mass
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 Tilmann Märk^{1,2}; *Ionicon Analytik, Innsbruck, Austria;
 *Universität Innsbruck, Innsbruck, Austria
- ThP 345 High Capacity Ion Trap Coupled to a Time of Flight MS for Comprehensive No-Loss MS/MS of All Stored Ions; Sunnie Myung¹; Andrew N. Kruchinsky²; David Fenyo¹; Julio Cesar Padovan¹; Herbert Cohen¹; Brian Chait¹; ¹The Rockefeller University, New York, NY; ²Department of Pharmaceutical Chemistry at UCSF, San Francisco, CA
- ThP 346 The Performance of a MALDI LTQ Orbitrap and its Application to the Study of Protein Complexes; Yang Luo; Tuo Li; Fang Yu; A. Chase Palish; Tal Kramer; Ileana M. Cristea; Princeton University, Princeton, NJ
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 A. Park²; Gary L. Glish¹; ¹University of North Carolina,
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- ThP 353 Direct Analysis of Biological Tissue by Electrospray
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- ThP 355 Improved Bioanalysis of Antidepressants from Plasma Using Non-Drip Filtration Plates; Eugene Chang; David Jones; Ritu Arora; Varian Inc., Lake Forest, CA
- ThP 356 A Simple Way to Remove Phospholipids from Bioanalytical Samples; Ben Yong¹; William Hudson¹; David Jones²; Yung-Lin Chen²; *Varian, Inc., Lake Forest, CA; *2Varian Inc., Lake Forest, CA
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- The Use of Liquid-Liquid Extraction along with Colloidal Silica and Polyvalent Cations to Remove Phospholipids that Produce ESI Matrix Effects; Dale Schoener; Stan Murakami; Alta Analytical Laboratory, El Dorado Hills, CA
- ThP 359 Biological Sample Phospholipids Clean Up: A
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- ThP 360 **Determination of Topiramate in Human Plasma**Using Negative Ion ESI-LC/MS/MS; Song Zhao;
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- ThP 361 Isolation of Digoxin from Human Plasma Using
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- ThP 363 Efficiency, Reproducibility, Accuracy and Linearity Evaluation of Filtration Plates during Protein Precipitation to Remove Phospholipids in Bioanalysis by LC-MS/MS; Catherine Dicaire; Milton Furtado; Fabio Garofolo; Algorithme Pharma Inc., Laval (Montreal), Quebec, Canada
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- ThP 366 Potential Ion Suppression from the Individual Components of Cannula Locking Solutions used in Rodent Studies; Daniel G. Morgan¹; Sarah J. Taylor¹; Marc Browning¹; Timothy Olah²; **Ibristol-Myers Squibb, Wallingford, CT; **Pristol-Myers Squibb Company, Lawrenceville, NJ
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- ThP 368 Maximizing Workflow Efficiency and Investigation of Drug Candidate Freeze/Thaw Recovery in Cerebrospinal Fluid After Addition of Plasma or Other Additives; Gary E. Adamson²; Debra Mcloughlin³; James Monahan¹; William Bart Emary⁴;

 ¹Merck Research Laboratories, West Point, PA; ²Merck and Co., West Point, PA; ³Merck & Co., West Point, PA; ⁴Merck Research Labs, West Point, PA
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- ThP 371 Diamond Nanoparticles for MALDI-TOF Mass Analysis of Bacterial Surface and Secretion Proteins; Chun-Wei Chen¹; Kai-Chih Chang^{2,3}; Anren Hu^{2,3}; Yen-peng Ho¹; Wen-ping Peng¹; ¹National Dong Hwa University, Shoufeng, Hualien, Taiwan; ²Tzu Chi University, Hualien, Taiwan; ³Buddhist Tzu Chi General Hospital, Hualien, Taiwan
- ThP 372 Combinatorial Metaproteomics and Metagenomics to Analyze Complex Bacterial Communities in situ;

 Nathanael Delmotte¹; Claudia Knief¹; Samuel
 Chaffron²; Bernd Roschitzki³; Gerd Innerebner¹;
 Christian von Mering²; Julia Vorholt¹; ^IETHZ, Zurich,

- Switzerland; ²University of Zurich, Zurich, Switzerland; ³Functional Genomics Center, Zurich, Switzerland
- ThP 373 Proteome Analysis of Iron-Corrosive Archaeon Methanococcus maripaludis OS7; Hanako Ataku; Miyako Mise; Keiko Nishijima; Jun Yamazaki; Jun Fukuda; Kazumi Sasaki; Syuji Yamazaki; Nobuyuki Fujita; Naofumi Ito; Satoshi Tanikawa; Hirohito Tsurumaru; Shigeaki Harayama; National Institute of Technology and Evaluation. Shibuya, Japan
- ThP 374 Investigating Potential Protein Functions of Small Unknown Reading Frames Secreted by Individual and Co-Cultured Thermophiles; Genna L. Andrews; Derrick L. Lewis; Sara E. Blumer-Schuette; Jaspreet Notey; Robert M. Kelly; Timothy S Collier; David C. Muddiman; North Carolina State University, Raleigh, NC
- ThP 375 Analysis of Botulinum Neurotoxin G Using Endopep-MS and Toxin Proteomics; Rebecca R Terilli¹; Hercules Moura⁵; Suzanne Kalb²; Adrian R Woolfitt³; Jon Rees³; Maribel Gallegos-Candela³; David M. Schieltz⁴; John R. Barr³; ¹Center for Disease Control and Prevention, Atlanta, GA; ²Centers for Disease Control and Prevention, Atlanta, GA; ³CDC, Atlanta, GA; ⁴Centers for Disease Control, Atlanta, GA; ⁵Centers for Disease Control and Prevention, Atlanta, GA
- ThP 376 Comprehensive Mass Spectrometric Analysis of Multiple Pertussis Toxins Reveals Amino Acid Coverage Homogeneity and Differential Subunit Expression; Yulanda M. Williamson; Hercules Moura; David M. Schieltz; Jon Rees; Adrian R. Woolfitt; Maria L. Tondella; Edwin Ades; Jacqueline S. Sampson; George Carlone; John R. Barr; Centers for Disease Control and Prevention, Chamblee, GA
- ThP 377 Identification of H7 Antigen of Escherichia Coli with Liquid Chromatography Tandem Mass Spectrometry (LC-MSMS); Keding Cheng; Joanne McCrea; David Lee; Katherine Sierks; Stuart McCorrister; Gary Van Domselaar; Helen Tabor; Garrett Westmacott; Gehua Wang; NML-PHAC Canada, Winnipeg, Canada
- ThP 378 In Planta Proteomics and Proteogenomics of the Biotrophic Barley Fungal Pathogen Blumeria graminis f.sp. hordei; Laurence V. Bindschedler¹; Tim Burgis²; Davinia J.S. Mills¹; Jenny Ho³; Pietro D. Spanu²; Rainer Cramer¹; ¹The University of Reading, Reading, UK, ²Imperial College London, London, UK; ³Thermo Fisher Scientific, Hemel Hempstead, UK
- ThP 379 Quantitative Proteomic Analysis of Gluconacetobacter Diazotrophicus Interaction with Sugarcane; Leticia Miranda Santos Lery¹; Eduardo M. Nogueira²; Paulo M. Bisch¹; Adriana S. Hemerly²; Wanda M. A. von Kruger¹; **Federal University of Rio de Janeiro, Rio De Janeiro, Brazil; **Instituto de Pesquisas do Jardim Botânico, Rio de Janeiro, Brasil
- ThP 380 Proteomic Analysis of Caulobacter Crescentus
 Outer Membrane Subproteome; Yuan Cao; Helen M.
 Johnson; Seth N. Levin; Carthene R. BazemoreWalker; Brown University, Providence, RI
- ThP 381 **Top-Down Identification of Bacterial Intact Protein Expression Profile Markers**; Melinda A. McFarland;
 John H. Callahan; Denis Andrzejewski; Rebecca Bell;
 Steven M. Musser; FDA/CFSAN, College Park, MD
- ThP 382 Decomposition of Soil Microbial Biomass: Investigations of Degradation Products by Mass Spectrometry; Adrian Spence¹; Andre J. Simpson²;

- Brian P. Kelleher¹; ¹Dublin City University, Dublin, Ireland; ²University of Toronto at Scarborough, Toronto, Canada
- ThP 383 Quantitative Mass Spectrometric Analysis Reveals Bacterial Cell-Wall Organization; Jiawei Chen¹; Gary J Patti²; Michael L. Gross¹; ^IWashington University, St Louis, MO; ²The Scripps Research Inst., La Jolla, CA
- ThP 384 Classification of Mycotoxin-Producing Fusarium Species Based on MALDI-TOF MS Analyses of their Intact Spores; Martina Marchetti-Deschmann¹; Wolfgang Winkler¹; Jasmin Kemptner¹; Emmanuel Raptakis²; Irina S. Druzhinina¹; Robert Mach¹; Christian P. Kubicek¹; Guenter Allmaier¹; *Vienna Univ. of Technology, Vienna, Austria; *2Shimadzu Biotech Kratos Analytical, Manchester, UK
- ThP 385 AP-MALDI MS/MS and Proteomics Based Rapid Detection of Food-Borne Pathogens; Appavu Sundaram; Seshu Gudlavalleti; Jane Razumovskaya; Vladimir M. Doroshenko; Science & Engineering Services, Inc., Columbia, MD
- ThP 386 Comprehensive Pathogen Identification Using MALDI TOF Coupled to Statistic Patented Procedure; Fan Xiang¹; Joachim Dyck²²², ¹Shimadzu Biotech, Pleasanton, CA; ²AnagnosTec, Potsdam, Germany
- ThP 387 Application of MS Signatures of Intact
 Microorganisms in the Search for Extant
 Extraterrestrial Life; Timothy J. Cornish¹; Plamen A.
 Demirev³; William Brinckerhoff⁴; Miquel Antoine⁵;
 Luann Becker²; Scott Ecelberger³; Jeffrey Lin³; Andrew Feldman³; Nathan Hagan³; ¹JHU/APL, MS:4-234,
 Laurel, MD; ²Johns Hopkins Univ., Baltimore, MD;
 ³JHU/APL, Laurel, MD; ⁴NASA Goddard SFC,
 Greenbelt, MD; ⁵JHU-APL, Laurel, MD
- ThP 388 Applicability of MALDI TOF Mass Spectrometry for Helicobacter Pylori Characterization and Typing; Elena Ilina¹; Marina V. Serebryakova¹; Alexandra D. Borovskaya¹; Kuvat T. Momynaliev¹; Thomas Maier²; Markus Kostrzewa²; <u>Vadim M. Govorun</u>¹; ¹Research Institute for Physical-Chemical Medicine, Moscow, Russian Federation; ²Bruker Daltonik GmbH, Bremen, Germany
- ThP 389 Investigating the Functional Activities and Cellular Processes of the Human Gut Microbiome by Multidimensional LC-MS/MS; Robert Hettich¹; Nathan C. Verberkmoes²; Alison Russell²; Manesh Shah¹; Mark Lefsrud⁶; Adam Godzik³; Claire Fraser-Liggett⁵; Janet Jansson⁴; *loak Ridge National Laboratory, Oak Ridge, TN; *luT-Oak Ridge National Lab, Knoxville, TN; *luT-Oak Ridge National Research, La Jolla, CA; *luwersity of Maryland School of Medicine, Baltimore, MD; *luversity, Quebec, Canada*
- ThP 390 Analysis of the Proteome Released through the Type III Secretion System (T3SS) of Burkholderia Species; Unige A. Laskay¹; Samanthi I Wickramasekara¹; Jennifer R. Bethke¹; Chengsi Huang¹; Mingshun Liu²; Imke Schroeder²; Todd French²; Jeff F. Miller²; Vicki H. Wysocki¹; ¹University of Arizona, Tucson, AZ; ²UCLA, Los Angeles, CA
- ThP 391 Metaproteomic Analysis of Microbial Endosymbionts from the Gutless Oligochaete Olavius Algarvensis; Jacque Young^{1,2}; Manuel Kleiner^{3,4}; Manesh Shah¹; Cecilia Wentrup⁴; Yun-Juan Chang¹; Christian Lott⁴; Stephanie Markert³; Nathan C.

- VerBerkmoes¹; Nicole Dubilier⁴; ¹Oak Ridge National Laboratory, Oak Ridge, Tennessee; ²University of Tennessee, Knoxville, TN; ³University of Greifswald, Greifswald, Germany; ⁴Max-Planck-Institute for Marine Microbiology, Bremen, Germany
- ThP 392 Systems Fluctuations of an Extremely Halophilic Archaeon Haloarcula Marismortui at Mid- and Late-Log Phase of Growth Analyzed by MS/MS; Lichieh Julie Chul¹; Han-ying Yang¹; Yihsuan Tsai²; Xuefeng Fung³; Ying Ting²; David R. Goodlett²; Wailap Ng¹; ¹National Yang Ming University, Taipei, Taiwan; ²University of Washington, Seattle, WA; ³Zhejiang University, Hangzhou, China

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- ThP 393 Structural Features of the Anti-HIV DNA
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 University, Changchun, China; ²Changchun Inst Appl
 Chem, Changchun, China
- ThP 394 Interaction of Oligonucleotide Sequence with Copper Complexes Using MALDI TOF Mass-Spectrometry; Alexander G. Majouga¹; Leonid A. Agron¹; Elena K. Beloglazkina¹; Nikolay I. Vorozhtsov¹; Ilya A. Agron²; Nina A. Khristenko²; Evgenij N. Nikolaev²; Nikolay V. Zyk¹; ILomonosov Moscow State University, Moscow, Russian Federation; Insitute for Energy Problems of Chemical Physics, Moscow, Russia
- ThP 395 Investigation of Structural Changes of Single Strand DNA Using Glyoxal and Potassium Permanganate Chemical Probes; Carol E. Parr¹; Jennifer Brodbelt²;

 ¹University of Texas, Austin, Austin, TX; ²The University of Texas, Austin, TX
- ThP 396 Probing Secondary and Tertiary Structures of
 Ribonucleoprotein Assemblies with Synthetic
 Deoxyribozymes; Kevin B. Turner; Micheal German;
 Arie Hawkins; Alberto Berton; Daniele Fabris; Univ. of
 Maryland, Baltimore County, Baltimore, MD
- ThP 397 Using Mass Spectrometry to Identify Components of Ribosome Assembly Intermediates; Romel Dator; Rebecca Rohlfs; Patrick A. Limbach; University of Cincinnati, Cincinnati, OH
- ThP 398 Accurate Mass Analysis of Oligonucleotides Using a High Resolution Orbitrap Mass Spectrometer; Amy Hilderbrand; Mark Sanders; Thermo Fisher Scientific, Somerset. NJ
- ThP 399 An Amide-HILIC Nano-LC/MS Based Platform for Oligonucleotide Profiling; Anders Mb Giessing¹; Finn Kirpekar²; ¹University of Southern Denma, Odense, Denmark; ²Univ. of Southern Denmark, Odense M, Denmark
- ThP 400 Rapid Characterization and Sequencing of RNAi
 Using Liquid Chromatography and Mass
 Spectrometry; Vera Ivleva²; Sean Mccarthy¹; Yingqing Yu²; Martin Gilar¹; **IWaters, Milford, MA; **2Waters
 Corporation, Milford, MA
- ThP 401 Bioanalytical Method Development for the Determination of Antisense Oligonucleotides in Mouse Plasma By Reverse Phase Ion-Pair LC-MS/MS; Philip S. Wong; Bruenner Bernd; Christopher James; Amgen, Thousand Oaks, CA
- ThP 402 Characterization of Degradation Pathways of Modified Therapeutic Oligonucleotides Using Mass Sequencing via UPLC MS; Ann O'brien; Merck Co Inc, West Point, PA

- ThP 403 Sequencing of Chemically Modified RNAs by
 Exonuclease Digestion and MALDI-TOF Mass
 Spectrometry; Hong Gao¹; Yong Liu¹; Megan
 Rumley²; Huimin Yuan¹; Bing Mao¹; ¹Merck & Co.,
 Inc., Rahway, NJ; ²Department of Chemistry, North
 Carolina State Univ, Raleigh, NC
- ThP 404 Investigating Nuclease Action in qPCR Using Fluorescence and Mass Spectrometric Detection; Eef Dirksen¹; Andrew Derome²; Kristiane Schmidt²;

 1 Philips Research, MiPlaza, Eindhoven, Netherlands;
 2 Philips Research, Molecular Diagnostics, Eindhoven, Netherlands
- ThP 405 Characterizing Quantifiable Signature Digestion Products of tRNAs by LC-MS/MS; Siwei Li; Colette Castleberry; Patrick A. Limbach; University of Cincinnati, Cincinnati, OH
- ThP 406 Electrospray-Generated Radical Cations as Negative Electron Transfer Dissociation (nETD) Reagents for Nucleic Acid Analysis; Teng-yi Huang; Scott A. Mcluckey; Purdue University, West Lafayette, IN
- ThP 407 Novel Software for Engineered/Hybrid Oligonucleotide Mass Spectrometry Data Analysis;

 Suping Zheng; Steven Becht; Xiaoya Ding; PPD, Inc., Middleton, WI
- ThP 408 Chemical Synthesis of Carboxymethylated DNA Lesions and LC-MS/MS for Assessing their Formation in DNA upon Exposure to Diazoacetate; Jianshuang Wang¹; Yinsheng Wang^{1,2}; ¹UC Riverside, Riverside, CA; ²University of California, Riverside, CA
- ThP 409 Mass Spectrometry for Revealing the Cytotoxic and Mutagenic Effects of the Minor Groove Adduct O²-Methylthymine in Cells; Nisana Andersen; Jianshuang Wang; Yinsheng Wang; University of California, Riverside, CA
- ThP 410 Mass Spectrometry for Assessing the Chemistry and Biology of DNA Lesions Formed from Byproducts of Glycolysis; Bifeng Yuan; Lei Xiong; Huachuan Cao; Yong Jiang; Yinsheng Wang; University of California, Riverside, CA
- ThP 411 Interloop Photoproduct Formation in the Human Telomere G-Quadruplexes; Dian Su; John-Stephen Taylor; Michael L. Gross; Washington University, St Louis. MO
- ThP 412 Analyses of Chemically Modified RNAs by Tandem Mass Spectrometry; Fanyu Meng; Huimin Yuan; Bing Mao; Merck & Co., Inc, Rahway, NJ
- ThP 413 Base Modification in Subtelomeric DNA Mass Spectrometric Analysis; Ilan Vidavsky¹; Michael L. Gross¹; Phillip Smiraldo²; Woodring E. Wright²; ¹Washington University, St Louis, MO; ²University of Texas Southwestern Medical Center, Dallas, TX
- ThP 414 Probing RNA Structure by Selective 2' Hydroxyl Acylation Analyzed by Mass Spectrometry (SHAMS); Alberto Berton¹; Kevin B. Turner¹; Robert G. Brinson^{2,3}; John P. Marino³; Stuart F.J. Le Grice²; Daniele Fabris¹; ¹Univ. of Maryland, Baltimore County, Baltimore, MD; ²National Cancer Institute, Frederick, MD; ³Center for Advanced Research in Biotechnology, Rockville, MD
- ThP 415 Ion Trap Collision-Induced Dissociation of Locked Nucleic Acids; Anastasia Kharlamova; Teng-yi Huang; Scott A. Mcluckey; Purdue University, West Lafayette, IN
- ThP 416 **Top-Down Mass Spectrometry of Modified RNA**; Monika Schöllnberger; Ulrike Rieder; Ronald Micura;

- Kathrin Breuker; University of Innsbruck, Innsbruck, Austria
- ThP 417 **Determination of Psoralen Binding to**Oligodeoxynucleotides by IRMPD and CID;
 Suncerae Smith; <u>Julia R. Aponte</u>; Jennifer Brodbelt;
 The University of Texas, Austin, TX
- ThP 418 Characterization of Interstrand Oligonucleotide Crosslinks by Infrared Multiphoton Dissociation;

 Sarah E. Pierce¹; Lynn J. Guziec²; Frank S. Guziec, Jr.

 ²; Jennifer S. Brodbelt¹; ¹The University of Texas,

 Austin, TX; ²Southwestern University, Georgetown, TX
- ThP 419 CID vs. ECD/ETD Sequencing of RNA:Protein Complexes; Kady Krivos¹; Patrick A. Limbach²;

 ¹University of Cinicinnati, Cincinnati, OH; ²University of Cincinnati, Cincinnati, OH
- ThP 420 An Efficient Strategy for the Identificiation of UVInduced Protein-RNA Crosslinks by ESI Mass
 Spectrometry; Florian Richter¹; He-Hsuan Hsiao¹;
 Nicodeme Paul²; Xiao Luo¹; Dimitry Agafonov¹;
 Reinhard Lührmann¹; Marcus Wahl¹; Mihaela
 Zavolan¹; Henning Urlaub¹; ¹MPI for Biophysical
 Chemistry, Goettingen, Germany; ²Biocenter of the
 University Basel, Basel, Switzerland

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- ThP 421 Quantitative Phosphoproteomics Study of the Sperm Membrane Protein During Capacitation; Han-Jia Lin²; Tin-Wei Lin¹²; Yu-Lun Chiu¹; <u>Yet-Ran Chen</u>¹²;

 **Academia Sinica, Taipei, Taiwan; **2National Taiwan Ocean University, Keelung, Taiwan
- ThP 422 Quantitative Phosphoproteomic Dissection of Signaling Pathways Applied to T Cell Signaling; Vinh Nguyen; Lulu Cao; Kebing Yu; Arthur Salomon; Brown University, Providence, RI
- ThP 423 Quantitative Phosphoproteome Analysis of a
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 Guo; College of Life Sciences, Wuhan University,
 Wuhan, Wuhan, China
- ThP 424 Phosphopeptide Profile for the Early Diagnosis of Minimal Residual Disease in Response to Doxorubicin Treatment of Leukemia Cell Disease; Songyun Xu; Stanford University, Palo Alto, CA
- ThP 425 Identification and Quantitation of GSK3

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 Factors; <u>David Cox</u>¹; Nathaniel B Nowacki²; John C

 McDermott²; ¹MDS Analytical Technology, Concord,
 Canada; ²York University, North York, Canada
- ThP 426 Quantitative Phospho-Proteomics of Human Embryonic Stem Cell Differentiation; Jeroen Krijgsveld^{1,4}; Javier Munoz¹; Dennis Van Hoof²; Martijn Pinkse¹; Stefan Braam^{2,5}; Rune Linding³; Christine Mummery^{2,5}; Albert J.R. Heck¹; ¹Utrecht University, Utrecht, The Netherlands; ²Hubrecht Institute, Utrecht, The Netherlands; ³Institute of Cancer Research, London, UK; ⁴EMBL, Heidelberg, Germany; ⁵Leiden University Medical Center, Leiden, The Netherlands
- ThP 427 Phosphorylation Dynamics of Kinases Across Mitosis; Kalyan Dulla; Henrik Daub; Renate Hornberger; Albert Ries; Erich Nigg; Roman Körner; Max Planck Institut für Biochemie, Martinsried, Germany
- ThP 428 Temporal Changes in Relative Protein Expression in Response to IGF-1R Signaling Using iTRAQ
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- **Cells**; <u>Patrick Murphy</u>¹; Devanand M. Pinto²; ¹Dalhousie University, Halifax, Canada; ²NRC, Halifax, NS
- ThP 429 Identification and Quantitative Profiling of
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 Gun Wook Park¹; Jeong Hwa Lee¹; Kyung-Hoon
 Kwon¹; Jinyoung Kim¹; Kyung Hee Byn²; Bong Hee
 Lee²; Jong Shin Yoo¹; ¹Korea Basic Science Institute,
 Ochang, South Korea; ²Gachon University Medical
 Center, Inchon, South Korea
- ThP 430 Quantitative Phosphoproteomic Analysis of Signaling Pathways Triggered by Insulin in Rat L6 Myotubes; Junjie Hou; Peng Xue; Zhensheng Xie; Ziyou Cui; Xiulan Chen; Peng Wu; Linan Shi; Tanxi Cai; Jing Li; Fuquan Yang; Institute of Biophysics, CAS, Beijing, China
- ThP 431 Analysis of Platelet Storage Lesion Signaling
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 Arash Khosrovi-Eghbal; Eva Rieker; Jason Rogalski;
 Juergen Kast; University of British Columbia,
 Vancouver, BC
- ThP 432 Characterising Corticotropin Releasing Hormone Receptor-Induced Signalling Dynamics; Georgios Efstathiou¹; Susan E Slade¹; Maria Delidaki¹; Jim Langridge²; Joanne B. Connolly³; Dimitri K Grammatopoulos¹; Chris Hughes³; James Scrivens¹;

 ¹Univ of Warwick, Coventry, UK; ²Waters Corporation, Manchester, UK; ³Waters, Manchester, UK
- ThP 433 Phosphoproteome Analysis of Pathogenic and Non-Pathogenic Pseudomonas Species; Yasushi

 Ishihama^{1,2}; Naoyuki Sugiyama¹; Sumiko Ohnuma¹;

 Masaru Tomita¹; Ayshwarya Ravichandran³; Sanjay
 Swarup³; Ikeio University, Tsuruoka, Japan; Presto-JST, Tokyo, Japan; National University of Singapore, Singapore
- ThP 434 Profiling Global Changes in the Phosphoproteome of Epithelial Cells Following the Inhibition of ERK1/2 MAP Kinase Pathway; Mathieu Courcelles; Catherine Julien; Sébastien Lemieux; Sylvain Meloche; Pierre Thibault; IRIC/Université de Montréal, Montréal, Canada
- ThP 435 Quantitative Site-Specific Tyrosine Phosphorylation Analysis of EphB Receptor Signaling; Guoan Zhang 13; David Fenyo²; Thomas Neubert 13; ¹Skirball Institute, NYUMC, New York, NY; ²The Rockefeller University, New York, NY; ³Skirball Institute, NYUMC, New York, NY
- ThP 436 Cdc5 Regulates Chromosome Condensation by Phosphorylation of the Condensin Complex; Julie St-Pierre; Mélanie Douziech; Franck Bazile; Mirela Pascariu; Eric Bonneil; Véronique Sauvé; Hery Ratsima; Damien D'Amours; IRIC-Université de Montréal, Montréal, QC
- ThP 437 Discovery of Anthrax Biomarkers Using Label-Free Quantitative Phosphoproteomics and LC-LTQ-Orbitrap-MS(/MS); Nathan P Manes; Li Dong; Weidong Zhou; Nikitha Reghu; Arjan C Kool; Charles Bailey; Emanuel F Petricoin; Lance A Liotta; Serguei G Popov; George Mason University, Manassas, VA
- ThP 438 Phosphorylation of p300 in the Beta-Catenin Interacting N-Terminus; Mingquan Guo; Zanxian Xia; Hong Ma; Nguyen Cu; Michael Kahn; University of Southern California, Los Angeles, CA

- ThP 439 Measurement of Kinase Profiles by Selected Reaction Monitoring; Ulrike Kusebauch¹; Johan Malmstroem²; Oliver Rinner²; Ruedi Aebersold^{1,2}; ¹Institute for Systems Biology, Seattle, WA; ²ETH, Zurich, Switzerland
- ThP 440 Characterization and Quantitation of Phosphotyrosine Signaling Networks: Selective Enrichment and Mass Spectrometry for Building Targeted Assays to Monitor Phosphorylation Cascades; Michael Major²; Michael Rosenblatt²; Paul Taylor¹; Scott Peterman²; Sarah Feuillerat²; Mark Schofield²; Barbara Kaboord²; John Rogers²; Michael Moran¹; Hospital for Sick Children, Toronto, ON;

 ²Thermo Fisher Scientific, Rockford, IL
- ThP 441 Ultrasensitive, Multiplexed Kinase Activity
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 Signaling Networks; Yonghao Yu¹; Rana Anjum¹;
 Kazuishi Kubota¹; John Rush²; Judit Villen¹; Steven
 Gygi¹; **Harvard Medical School, Boston, MA; **2Cell Signaling Technology, Danvers, MA**
- ThP 442 Development and Application of a Label-Free Quantitative Phosphoproteomic Platform to Study Signaling Pathways in Zebrafish; Erik J. Soderblom¹; J. Will Thompson¹; Melanie Philipp^{1,2}; Marc G. Caron^{1,2}; Arthur Moseley¹; **Duke University School of Medicine, Durham, NC; **Department of Cell Biology, Durham, NC
- ThP 443 A Combined SIMAC-HILIC-TiO₂ Strategy for Large-Scale Phosphoproteomic Analysis of Sub-Milligram Amounts of Sample Material; <u>Kasper Engholm-Keller</u>; Søren S. Jensen; Martin R. Larsen; *University of Southern Denmark, Odense M, Denmark*
- ThP 444 Can SILAC Quantitatively Characterize Phosphoproteome in Culture Cells?; Koshi Imami¹; Naoyuki Sugiyama¹; Masaru Tomita¹; Yasushi Ishihama¹.²; Institute for Advanced Biosciences, Keio Univ., Tsuruoka, Japan; Presto, Tokyo, Japan
- ThP 445 Analysis by Blue Native PAGE and Mass
 Spectrometry of Protein-Protein Interactions within
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 Zhang⁵; Kathrin Deinhardt²; Vivekananda Shetty³;
 Thomas Neubert²; ¹The Mount Sinai Medical Center,
 New York, NY; ²Skirball Institute, NYUMC, New York,
 NY; ³Immunotope, Inc., Doylestown, PA; ⁴Merck & Co.,
 Rahway, NJ; ⁵New York University, New York, NY
- ThP 446 Highly Multiplexed Robust Phosphopeptide
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 MRM Methods; Brigitte Simons¹; Jason Hoffert²;
 Mark Knepper²; IMDS Analytical Technologies,
 Concord, Canada; NHLBI, Bethesda, MD
- ThP 447 A Systematic Approach to Identify Protein Kinase Substrates; Yong Chi^{1,2}; Jeffrey J. Posakony²; Bruce E. Clurman²; Ruedi Aebersold¹; Institute for Systems Biology, Seattle, WA; Fred Hutchinson Cancer Research Center, Seattle, WA
- ThP 448 High Sensitivity Nanoscale Multidimensional LC/MS Analysis of Phosphopeptides; Scott Ficarro¹; Yi Zhang¹; Feng Zhou¹; Job Cardoza¹; Guillaume Adelmant¹; Manor Askenazi²; Amanda Berg³; Gary Valaskovic³; Jarrod Marto¹; ¹Dana-Farber Cancer Institute, Boston, MA; ²Dana-Farber Cancer Institute and Hebrew University, Boston, MA; ³New Objective, Inc., Woburn, MA
- ThP 449 Selective Elution of Singly and Multiply Phosphopeptides in Aliphatic Hydroxy Acid-

- **Modified Metal Oxide Chromatography**; <u>Yutaka Kyono</u>¹; Naoyuki Sugiyama¹; Masaru Tomita¹; Yasushi Ishihama^{1,2}; *^TKeio University*, *Tsuruoka*, *Japan*; ²*Presto JST*, *Tokyo*, *Japan*
- ThP 450 Quantitative Phosphoproteome Analysis of the TNF-Signaling Protein having Biphasic Phos-tag/C18 Tip Separation between iTRAQ-Labeling and MS Analysis; Takuji Nabetani¹; Yeon-Jeong Kim¹; Masaki Watanabe²; Yoko Ohashi¹; Hiroyuki Kamiguchi¹; Yoshio Hirabayashi¹, **Iriken BSI, Wako, Japan; **IHitachi High-Technologies, Hitachinaka-shi, Japan
- ThP 451 A New Approach for Quantitative
 Phosphoproteomic Dissection of Signaling Pathways
 Applied to T Cell Receptor Activation; Vinh
 Nguyen¹; Arthur Salomon²; ¹Brown University MCB
 Department, Providence, RI; ²Brown University,
 Providence, RI
- ThP 452 Molecular Dissection of Ras-MAPK Signaling
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 Therrien; Pierre Thibault; Univ. of Montreal, Montreal,
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- ThP 453 Phosphopeptide Analysis of Marek's Disease Virus (MDV)-Infected Cells Using Electrostatic Repulsion Hydrophilic Interaction Chromatography (ERLIC), IMAC, and LC/MS/MS; Ko-yi Chien; Kevin Blackburn; Hsiao-Ching S. Liu; Michael B. Goshe; NC State University, Raleigh, NC
- ThP 454 Enrichment and 12-Plex Profiling of
 Phosphoproteins Using Affinity Chromatography,
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 Rosenblatt¹; Michael Major¹; Julian Saba²; Sarah
 Feuillerat¹; Rosa Viner²; Krystal Rampalli¹; John
 Rogers¹; Thermo Fisher Scientific, Rockford, IL;
 ThermoFisher Scientific, San Jose, CA

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- ThP 455 New Insights into the Degradation of Neuropeptides by Metalloendopeptidases; Markus Hardt¹; Richard Niles²; Graeme S. Cottrell²; Nigel Bunnett²; ¹Boston Biomedical Research Institute, Watertown, MA; ²Univ. of CA San Francisco, San Francisco, CA
- ThP 456 Characterization of Drosophila Melanogaster Neuropeptides by MALDI-FT-ICR Imaging MS, MALDI-TOF MS, and MALDI-TOF/TOF MS;

 Kristin J. Boggio¹; Yun-Wei A. Hsu¹; Paul J. Kowalski²; Michael L. Easterling²; Michael Rosbash¹; Jeffrey N. Agar¹; **IBrandeis University, Waltham, MA; **2Bruker Daltonics Inc., Billerica, MA**
- ThP 457 Use of an Antibody Functionalized Surface Specific for Amyloid Precurser Protein in Detection of Beta Amyloid Fragments by Mass Spectrometry; Steve Roth^{1,1}; Vanitha Thulasiraman^{1,2}; Amanda Bulman^{1,2}; Fiona Plows^{1,3}; Mariana Rusa^{1,2}; Matthew Hammond^{1,4}; Fremont, CA; ²Bio-Rad Laboratories, Hercules, CA; ³Bio-Rad Laboratories, Inc., Hercules, CA; ⁴Stanford University, Stanford, CA
- ThP 458 Mapping Neuropeptide Expression in Single Identified Neurons in the Nematode Ascaris Suum;

 Jessica Jarecki; Kari Andersen; Martha M. Vestling;
 Antony O. Stretton; University of Wisconsin, Madison,
 WI
- ThP 459 C-Terminal Methyl Esterification During
 Neuropeptide Extraction; Elizabeth A. Stemmler¹;
 Elizabeth E. Barton¹; Laura L. Onderko¹; Andrew E.
 Christie²; Patsy S. Dickinson¹; **IBowdoin College,**

- Brunswick, ME; ²Mount Desert Island Biological Laboratory, Salisbury Cove, ME
- ThP 460 Exploring the Functional Consequences of Neuropeptide Diversity by MALDI Mass Spectrometry; Limei Hui; Ruibing Chen; Lingjun Li; Univ. of Wisconsin-Madison, Madison, WI
- ThP 461 MS-Based Characterization of Neuropeptides
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 Nucleus; Shifang Ren; Norman Atkins; Ji Eun Lee;
 Nathan G. Hatcher; Martha U. Gillette; Neil L.
 Kelleher; Jonathan Sweedler; University of Illinois at
 Urbana-champaign, Urbana, IL
- ThP 462 Using Deuterium Exchange Electrospary Mass Spectrometry to Evaluate Inhibitors of Amylooid-β Oligomerization; Zijuan Zhang; Jason J. Evans; Marrianna Torok; University of Massachusetts Boston, Boston, MA
- ThP 463 **High Throughput Single Cell MALDI-MS**; <u>Stanislav Rubakhin</u>¹; Jonathan Sweedler², ¹Beckman Institute, UIUC, Urbana, IL, ²University of Illinois, Urbana, IL
- ThP 464 Characterization of Signaling Peptides in Sensory
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 Spectrometry; Elena V. Romanova¹; Stanislav S.
 Rubakhin¹; Ferdinand S. Vilim²; Jonathan V.
 Sweedler¹; ¹University of Illinois, Urbana, IL, ²Mount
 Sinai School of Medicine, New York, NY
- ThP 465 Development and Application of Quantitation via In Cell Combination (QUICC) Methodology for MALDI FTMS Analysis of Neuropeptides in Environmental Stress; Yuzhuo Zhang; Ruibing Chen; Lingjun Li; University of Wisconsin, Madison, WI
- ThP 466 Discovery of Novel Neuropeptides and Processing Mechanisms Using Mass Spectrometry; Nitin Gupta; Steven Bark; Weiya Lu; Laurent Taupenot; Daniel O'Connor; Pavel Pevzner; Vivian Hook; UCSD, La Jolla, CA
- ThP 467 MALDI-MS Probing of Non-Covalent Protein Complexes Related to Alzheimer's Disease; Basri Gülbakan¹; Bekir Salih²; ¹University of Florida, Gainesville, Florida; ²Hacettepe University, Ankara, Turkey
- ThP 468 Peptidomic Profiling of Secreted Products from Cardiomyocytes Reveals Novel Natriuretic Peptide Processing; Nancy Andon; James Bilakovics; Svetlana Nikoulina; Kevin McCowen; Steven Taylor; Amylin Pharmaceuticals, Inc., San Diego, CA
- ThP 469 Expression and Distribution of Neuropeptides in the Nervous System of the Lobster Homarus Americaus and their Roles in Development; Ruibing Chen; Xiaoyue Jiang; Lingjun Li; UW, Madison, Madison, WI
- ThP 470 In vivo Monitoring of Dose Dependent Dynamic Changes of Endogeneous Enkephalins by Microdialysis with Capillary LC Multistage MS;

 Oiang Li; Jon-Kar Zubieta; Robert Kennedy; University of Michigan, Ann Arbor, MI
- ThP 471 Inhibition of Prohormone Convertase 1/3 Peptide
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 David Cool; Wright State University, Dayton, OH

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Michael J Treuheit; David Brems; Da Ren; Amgen Inc.,
Thousand Oaks, CA

- ThP 473 Identification of Protein Differences in the *C.elegans*Insulin Signaling Pathway; Gennifer Merrihew;
 Gregory L. Finney; Michael J. Maccoss; *University of Washington, Seattle, WA*
- ThP 474 Novel Interacting Partners of the Escherichia Coli Poly(A) Polymerase I (PAPI): in vivo Evidence for Interaction with the Degradosome; Valerie J.

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- ThP 476 Redox-Dependent Disulfide Formation in the Zinc-Finger Motif of the SAP30L Co-repressor Protein Studied by ESI FT-ICR Mass Spectrometry; Janne Jänis¹; Mikko Laitaoja¹; Keijo Viiri²; Jarkko Valjakka²; Olli Lohi²; Perttu Permi³; Tero Pihlajamaa³; Helena Tossavainen³; Pirjo Vainiotalo¹; ¹University of Joensuu, Joensuu, Finland; ²University of Tampere, Tampere, Finland; ³University of Helsinki, Helsinki, Finland
- ThP 477 Analysis of Cross-Linked Cu/Zn-Superoxide
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 Dagmar Ringe; Gregory A. Petsko; Jeffrey N. Agar;
 Brandeis University, Waltham, MA
- ThP 478 Complexes of Perfluorooctanoic Acid (PFOA) and Liver Fatty Acid Binding Protein Probed by Electrospray-Tandem Mass Spectrometry (ESI-MS/MS); Raymond E. March¹; Naomi L. Stock²; Kyle Trumpour¹; Mark Woodcroft³; Steven P. Rafferty¹; David A. Ellis¹.⁴; ¹Department of Chemistry, Trent University, Peterborough, Canada; ²Worsfold Water Quality Centre, Trent University, Peterborough, Canada; ³Department of Biochemistry, Queen's University, Kingston, Canada; ⁴Canadian Environmental Modelling Centre, Peterborough, Canada
- ThP 479 Utilization of a Flow through Membrane
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 Bergman²; Hans Jornvall²; Thorleif Lavold³; Craig M.
 Whitehouse¹; ¹Analytica of Branford, Inc., Branford,
 CT; ²Karolinska Institutet, Stockholm, Sweden;

 ³Biomotif AB, Danderyd, Sweden
- ThP 480 Mass Spectrometry-Based Footprinting of HIV-1
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 Christopher Mckee; Jacques J. Kessl; Jocelyn O.
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 Ohio State University, Columbus, OH
- ThP 481 Qualitative and Quantitative Analysis of Programmed Ribosomal Frameshifting by Multiple Reaction Monitoring; Yong Seok Choi¹; Pei-Yu Liao²; Kelvin H. Lee¹; ¹University of Delaware, Newark, DE; ²Cornell University, Ithaca, NY
- ThP 482 Reconstituted Nucleosomes Containing
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 University of Pennsylvania, Philadelphia, PA
- ThP 483 Thermodynamic Analysis of Protein-Ligand Binding Interactions Using SPROX; Graham M West;

- Stephanie Cordato; Michael C. Fitzgerald; *Duke University, Durham, NC*
- ThP 484 Elucidation of the Binding of Abeta 1-40 with Human Apolipoprotein E3 by FPOP Labeling; Brian C. Gau; Michael L. Gross; Washington University, St. Louis MO
- ThP 485 Rapid, Isotope-Coded Method for Mapping Protein-Protein and Protein-Ligand Interactions; Katina L Johnson; Matthew J Cuneo; Robert E London; Kenneth B Tomer; Jason G Williams; NIEHS, NIH, DHHS, Research Triangle Park, NC
- ThP 486 Identification of Gli2 Protein Complexes in Mammalian Cells Using Nano-LC-MSMS and MALDI-TOF/TOF; Min Du; Ke Lu; Charles P. Emerson; Boston Biomedical Research Institute, Watertown, MA
- ThP 487 **Biochemical and Functional Characterization of**Serine Protease HTAR1 in Human Retinal Pigment
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 Sen²; Heather Gordish-Dressman²; Kristy J. Brown²;
 Yetrib Hathout²; ¹The George Washington University,
 Washington, DC; ²Children's National Medical Center,
 Washington, DC
- ThP 488 States of DNA Packaging Motors in Bacteriophage:
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- ThP 489 Protein Interactions of the Telomerase Holoenzyme in Saccharomyces Cerevisiae and Schizosaccharomyces Pombe; Karin R. McDonald; Virginia A. Zakian; Ileana M. Cristea; Princeton University, Princeton, NJ
- The CrkRS/CDK12 Kinase is Activated by a Novel Isoform of Cyclin K and Phosphorylates the C-Terminal Domain of RNA Pol2; Annie Moradian¹; Michael Kuzyk²; S.-W. Grace Cheng¹; Jerry Tien³; Emily Schaeffer³; Gregg Morin^{1,3}; **Igenome Sciences Centre, BC, Vancouver, Canada; **2University of Victoria Genom, Victoria, BC; **3University of British Columb, Vancouver, BC
- ThP 491 **Profiling Akt-Interacting Proteins in Neuronal Cells**; Bill Huang; Hee-yong Kim; National Institutes of Health, Bethesda, MD
- ThP 492 Using Different Mass Spectrometry Approaches to Study PKA Interactome; Yurong Guo¹; Yuliang MA¹; Susan S Taylor^{1,2}; ¹HHMI, San Diego, CA; ²UCSD, San Diego, CA
- ThP 493 **Beam-type CID of Whole Protein Ions in Excess of** 35 kDa; Chamnongsak Chanthamontri; Scott A. Mcluckey; *Purdue University, West Lafayette, IN*
- ThP 494 **Optimization and Evaluation of Subcellular Fractionation Method for Global Proteomic Analysis**; <u>Jong-won Kim</u>; *Monarchlifesciences*, *Indianapolis*, *IN*
- ThP 495 Mass Defect Analysis of Tryptic Peptides from Human Biofluids: A Fresh Look; Melinda L Toumi; Heather Desaire; University of Kansas, Lawrence, KS
- ThP 496 Evaluation of Dynamic Range of Protein Identification and Quantification by LC-MSMS Using a Proteomics Dynamic Range Standard Mixture; Suya Liu; Gilles Lajoie; University of Western Ontario, London, ON, Canada
- ThP 497 Cleavable Affinity Extraction and Mass Spectrometric Analysis of Small Molecule-Binding Proteins; Nariyasu Mano^{1,2}; Koichi Sato²; Kohei

- Abe^{1,2}; Masaru Mori²; Hiroaki Yamaguchi^{1,2}; Takaaki Goto²; Miki Shimada^{1,2}; Junichi Goto¹; ¹Tohoku University Hospital, Sendai, Japan; ²Tohoku University, Sendai, Japan
- ThP 498 Study of Proteolytic Digestion Efficiencies Under Conventional Heating and Microwave Irradiation Using MALDI-MS; Chia-chen Chen; Mei-chuan Sun; Jun-Fu Hu; Yen-Peng Ho; National Dong Hwa University, Taipei, Taiwan
- ThP 499 High-Speed, High-Resolution Antibody Analysis
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 Scott Anderson; Mark Jacyno; Wendy Luo; Ian
 Chappell; Grace Davison, Deerfield, IL
- ThP 500 **Temperature Effect on Ultrasound-Assisted Tryptic Digestion of Proteins**; Seongjae Shin; Jinhee Kim;
 Hyo-jik Yang; Gae Ho Lee; Jeongkwon Kim;
 Chungnam National University, Daejeon, South Korea
- ThP 501 Finding the Needles in the Hay Stack Identifying Interacting Regions through Cross-Linking; A.

 Jimmy Ytterberg¹; Elena E. Grintsevich²; Dmitri S.

 Kudryashov²; Zeynep A. Oztug Durera²; Emil Reisler²;

 Ole N. Jensen¹; Joseph A. Loo²; ¹University of Southern Denmark, Odense, Denmark; ²UCLA, Los Angeles, CA
- ThP 502 Evaluation of Cross-Linker and Protein Dynamics in Cross-Linking Coupled to Mass Spectrometry Experiments; Alana Dos Reis Figueiredo; Paulo C. T. Souza; Munir S. Skaf; Fabio C Gozzo; Institute of Chemistry University of Campinas, Campinas, Brazil
- ThP 503 Protein Footprinting by Peroxide Photolysis Using Hg Lamp and 213 nm Laser as Radiation Sources; Eduardo J Pilau; Alexandre F. Gomes; Marcelo A. O. Silva; Marco Aurelio Z. Arruda; Fabio C Gozzo; IQ-University of Campinas, Campinas, Brazil
- ThP 504 Use of Marker Ions and High Resolution Precursor Ion Scan for the Identification of Cross-linked Peptides; Fabio C Gozzo; Amadeu H Iglesias; Luiz Fernando Arruda Santos; IQ University of Campinas, Campinas, Brazil
- ThP 505 Enhanced Detection of Intact Proteins by Nanolc-MS Using a Novel Trapping Mode on a Hybrid Linear Ion Trap Mass Spectrometer; Paul Drogaris^{2,6}; Feng Zhong¹; J.c. Yves Leblanc¹; Alain Verreault^{2,4}; Jennifer Fitzgerald⁵; Noel Lowndes⁵; Pierre Thibault^{3,6}; ¹MDS Analytical Technologies, Concord, ON, Canada; ²Université de Montréal, Montréal, QC; ⁴Dept.Pathology & Cell Biology (U de Montreal), Montreal, Canada; ⁵Dept. Biochemistry National University of Ireland, Galway, Ireland; ⁶Institue for Research in Immunology and Cancer, Montreal, Canada
- ThP 506 Extraction and Identification of Proteins from a Pottery Matrix Using Microwave-Assisted Enzymatic Digestion and Tandem Mass Spectrometry; Andrew Barker²; Steve Wolverton²; Barney Venables²; Stanley M. Stevens, Jr. ¹; ¹University of South Florida, Tampa, FL, ²University of North Texas, Denton, TX
- ThP 507 Specific Non-covalent Complex between the Major-Sperm-Protein Homology Domain of a Vesicle-Associated-Membrane-Protein-Associated Protein (VAP) and FFAT-Motif Peptides in the Gas Phase;

 Thomas A. Shaler¹; Stephen E. Kaiser²; Chris Becker¹;

 PPD Biomarker Discovery Sciences, Menlo Park, CA;

 Stanford University, Stanford, CA

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- 1 Receptor Using Novel Affinity Ligand Purification
- **Decipher Both Stable and Transient Interactors of** Membrane Proteins in Yeast Peroxisomes; Silke Oeljeklaus¹; Benedikt S. Reinartz¹; Michael Kohl¹; Christian Stephan¹; Ralf Erdmann²; Helmut E. Meyer¹; Bettina Warscheid¹; ¹Medizinisches Proteom-Center, Bochum, Germany; ²Department for Systems Biochemistry, Bochum, Germany
- ThP 515 **Comprehensive Proteomic Analysis of Yersinia** Pestis Membrane Proteins; Moo-Jin Suh¹; Rembert Pieper¹; Shih-Ting Hung¹; David J. Clark¹; Jeffrey M. Robinson¹; Hamid Alami¹; Prashanth P. Parmar¹; Srilatha Kuntumalla¹; Christine L. Bunai¹; Robert D. Perry²; Robert D. Fleischmann¹; Scott N. Peterson¹; ¹J Craig Venter Institute, Rockville, MD; ²Department of Microbiology, University of Kentucky, Lexington, KY
- ThP 516 **Quantitative Proteomics Analysis of Cell Surface** Caveolae in Mammary Epithelial Tumor Cells; Yu Zi Zheng; Ivan R. Nabi; Leonard J. Foster; University of British Columbia, Vancouver, Canada
- ThP 517 Analysis of the Membranome of Breast Cancer Cell **Lines by Comparative Shotgun Proteomics** Identifies Tumor Associated Antigens; Lori C Stansberry; Eberhard Durr; Mark A Miller; Joseph G. Joyce; Loren D. Schultz; Merck and Co., West Point,
- ThP 518 The Membrane Topology and the Dynamics of Melittin within the Liposomes; Kazumi Saikusa; Yo

Hiroshima University, Higashihiroshima, Japan ThP 519 **Determination of Membrane Protein Topology Expressed in a Wheat Germ Cell-Free Expression**

Kono; Shunsuke Izumi; Graduate School of Science,

- System Using Proteolysis Reactions and Mass Spectrometry; Mark Scalf; Michael A. Goren; Mathew R. Lockett; Brian G. Fox; Lloyd M. Smith; University of Wisconsin, Madison, WI
- ThP 520 A Structural Investigation into the CB2 Receptor Using Covalent Ligands; Dennis Szymanski¹; Malvina Papanastasiou²; Alexander Makriyannis¹; ¹Center for Drug Discovery, Boston, MA; ²Northeastern University, Boston, MA
- Proteomics Analysis of Mitotic Golgi Disassembly ThP 521 and Reassembly Using a Reconstitution System; <u>Xuequn Chen¹</u>; Eric Simon²; Maureen Kachman²; Yanzhuang Wang¹; Philip Andrews²; ¹The University of Michigan, Ann Arbor, MI; ²University of Michigan, Ann Arbor, MI
- ThP 522 Observation of Processed Proteins by ID Gel LC-MS/MS and Scaffold Data Visualization Software; Randy J. Arnold; Rohini R. Kohli; Richard W. Hardy; Indiana University, Bloomington, IN
- ThP 523 Investigation of Protein Interactions of Gamma-Glutamyl Carboxylase and Vitamin K-Dependent Substrates Using Covalent Crosslinking and Mass **Spectrometry**; Christine Hebling; James Jorgenson; University of North Carolina, Chapel Hill, NC
- ThP 524 **Efficiency Comparison of Magnetic and** Conventional Protein A/G Beads for Membrane Protein Immunoprecipitation for MS Analysis; Hui Jiang; Alexis Ramos; Xudong Yao; Department of Chemistry, University of Connecticut, Storrs, CT
- ThP 525 Approaching the Complexity of Membrane Proteomes Digested with Elastase Using IEF/nLC-MALDI-MS/MS; Benjamin Rietschel¹; Tabiwang N. Arrey¹; Bjoern Meyer¹; Sandra Bornemann¹; Dimitrios Papasotiriou¹; Ansgar Poetsch²; Michael Karas¹; ¹University Frankfurt, Frankfurt, Germany; ²University Bochum, Bochum, Germany
- ThP 526 **In-Gel Digestion of Mouse Membrane Protein** Extract: 85% Increase in Peptide Recovery and Identification of Very Low Abundance Hydrophobic **Proteins**; Chris Adams¹; Allis S. Chien¹; Daniel J. Simpson²; Bill Dailey²; Sergei Saveliev²; ¹Stanford University, Stanford, CA; ²Promega Corp., Madison,
- ThP 527 Development of LC and LC-MS/MS Methods for the Analysis of p14 Fusion-Associated Small Transmembrane Protein; Reno Nguyen¹; Wendy <u>Luo</u>¹; Roberto de Antueno²; Roy Duncan²; *Grace* Davison Discovery Scie, Deerfield, IL; ²Dalhousie University, Nova Scotia, Canada
- ThP 528 **Sequential Gel-Assisted Digestion for Concomitant** Analysis of Phosphorylated and Glycosylated Membrane Proteome; Chih-Wei Chien¹; Chia-li Han²; Chia-feng Tsai²; Yi Ting Wang²; Yu-ju Chen²; ¹Dep. of Chemistry National Tsing Hua Univercity, Hsinchu, Taiwan; ²Institute of Chemistry, Academia Sinica, Taipei, Taiwan
- ThP 529 **Determination of GTPase Expression in Membrane** and Cytosolic Fractions after Bisphosphonate Treatment; Marjo Jauhiainen^{1,3}; Seppo Auriola¹; Hannu Mönkkönen^{1,2}; Michel Boutin³; Jukka Mönkkönen¹; Pierre Thibault³; ¹University of Kuopio, Kuopio, Finland; ²INSERM, Universite Claude Bernard

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William S. Hancock; Northeastern University, Boston,

Mazzeo¹; Asish Chakraborty¹; Weibin Chen¹; Waters Corporation, Milford, MA; ²Dept. of Pharmacy, The

Netherland Cancer Inst, Amsterdam, The Netherlands

Recombinant Protein Samples; Wendy L. White; Jon

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- ThP 552 Characterization of a Novel Amine Derivatization to Investigate the Structural Properties of Proteins by Mass Spectrometry; Lake N. Paul; Kenneth B. Tomer; NIEHS, Raleigh, NC
- ThP 553 Lysine-Methylation: Mass Spectrometric
 Approaches for the Identification of Modified
 Proteins; Rosalind Yc Tan; Manfred R. Raida; ChoonKeow Ng; Bernard PM Tham; Experimental
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- ThP 554 Mapping Iodination Sites of Whole Proteins by MALDI-MS and Gas Phase Photodissociation;

 Oingyu Sun; Ryan R. Julian; University of California, Riverside, CA

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 14 and 28 Da Mass Shifts Detected by MALDI-MS
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 CAMS & PUMC, Beijing, China
- ThP 556 Enhanced Peptide Peak Intensity with the use of Cysteine Modifiers and MALDI-TOF/TOF for Improvement of Protein Identification; Masoud Zabet Moghaddam; Satomi Niwayama; Texas Tech University, Lubbock, TX
- ThP 557 Liquid Chromatography/Mass Spectrometric
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 Ying Zhang; Brian Wiggins; Shujun Bai; Lihe Su; Yen-Ming Hsu; Alex Buko; Sharon Gao; Biogen Idec, San Diego, CA
- ThP 559 Optimizing the Kinetics of the Indirect Oxidation Pathway for an Electrochemistry-Based Protein Surface Mapping Pipeline; Paul Abraham; Carlee Mcclintock; Jerry Parks; Vilmos Kertesz; Robert Hettich; Oak Ridge National Laboratory, Oak Ridge, TN
- ThP 560 Accurate Evaluation of Transcription Factor
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 Seeholzer; Gerd Blobel; Children's Hospital of
 Philadelphia, Philadelphia, PA
- ThP 561 Using Mass Spectrometry to Characterize the Novel Disulfide Linkage in the Endonuclease Motif of the Arabidopsis CPSF30 Ortholog; Balasubrahmanyam Addepalli¹; Arthur G. Hunt²; Patrick A. Limbach¹;

 ¹University of Cincinnati, Cincinnati, OH; ²University of Kentucky, Lexington, KY
- ThP 562 A Mass Spectrometric Comparison of the Interactions of Cisplatin and Transplatin with Myoglobin; Ting Zhao; Fred King; West Virginia Uni, Morgantowm, WV
- ThP 563 In vitro glycation of glyoxalase II by methylglyoxal Characterization of the glycation sites of by LC/MS/MS; Jean Pierre Le Caer; Olivier Laprevote; Naima Nhiri; Eric Jacquet; Jean-Yves Lallemand; CNRS Institut de Chimie des Substances Naturelles, Gif sur Yvette, France
- ThP 564 Role of Hemoglobin Oxidation in the Formation of the Red Blood Cell Storage Lesion; <u>Grady Blacken</u>; Yi Wang; Ryan Gallagher; Xiaoyun Fu; <u>Puget Sound Blood Center</u>, <u>Seattle</u>, <u>WA</u>
- ThP 565 Identification of Candidate Plasma Biomarkers for Diabetic Complications: In vivo Methylglyoxal Modified Hotspots; Mike Kimzey²; Michael A Galligan²; Hussein Yassine²; Craig Stump²; George Tsaprailis²; Serrine S. Lau¹, ¹Univ of Arizona, Pharmacy, Tucson, AZ; ²University of Arizona, Tucson, AZ
- ThP 566 Characterization of the Conjugation Sites in
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- ThP 567 Elucidation of PEGylation Site with a Combined Approach of In-Source Fragmentation and CID

- MS/MS; Xiaojun Lu; P. Clayton Gough; Michael R. DeFelippis; Lihua Huang; Eli Lilly and Company, Indianapolis, IN
- ThP 568 Probing the Structure of the Gram-Positive Ribosome with Chemical Labeling; Matthew A.

 Lauber; William E. Running; James P. Reilly; Indiana University, Bloomington, IN
- ThP 569 Top-down and Bottom-up Analysis of Nitrated Proteins by ECD, CID and IRMPD Mass Spectrometry; Victor A. Mikhailov¹; Andrew W. Jones¹; Jesus Iniesta²; Helen Cooper¹; ¹University of Birmingham, Birmingham, UK; ²University of Alicante, Alicante, SPAIN
- ThP 570 Verification of Selenomethionine Incorporation by Top-Down and Bottom-Up Mass Spectrometry; Xu Wang 1.2; Jeremiah Tipton2; Mark R. Emmett2; Alan G. Marshall 1.2; I Florida State University, Tallahassee, FL; Nat'l High Magnetic Field Lab, Tallahassee, FL
- ThP 571 Development of a Microfluidic Quench-Flow Interface Compatible with ESI-FT-ICR MS for the Characterization of Enzyme Mechanisms; David J Clarke; Adam A. Stokes; Pat Langridge-smith; C. Logan Mackay; SIRCAMS, Dept. Chemistry, University of Edinburgh, Edinburgh, U.K.
- ThP 572 Characterization of PEGylated-Peptides and Site Localization of Attachment with High Resolution ETD Mass Spectrometry; Andrew Carr¹; Tonya Second²; Robert Cummins¹; Rosa Viner³; Lihua Huang¹; ¹Eli Lilly and Company, Indianapolis, IN; ²Thermo Fisher Scientific, San Jose, CA; ³ThermoFisher Scientific, San Jose, CA
- ThP 573 Redox-Regulation of p53: Identification of Redox Modifications Using Top Down FT-ICR Mass Spectrometry; Jenna Scotcher¹; David J Clarke¹; Penka Nikolova²; Ted Hupp³; Peter Sadler⁴; Pat Langridge-Smith¹; C. Logan Mackay¹; ¹SIRCAMS, Dept. Chemistry, University of Edinburgh, Edinburgh, UK; ²Dept. Biochemistry, King's College London, London, UK; ³University of Edinburgh Cancer Center, Edinburgh, UK; ⁴Dept. Chemistry, University of Warwick, Coventry, UK
- ThP 574
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- ThP 575 FT-ICR MS Identification of Non-Pathologic Oxidative Modifications on Creatine Kinase in Alzheimer's and in Control Brains; Shannon M. Eliuk; Matthew B. Renfrow; Stephen Barnes; Helen Kim; University of Alabama at Birmingham, Birmingham, AL
- ThP 576 Probing Critical Quality Attributes of an IgG2 mAb via Characterization of Forced Degradation
 Samples; Xin Zhang; Liping Chu; Hung Tran; Andrew Goetze; Jette Wypych; Amgen. Thousnad Oaks, CA
- ThP 577 Characterization of S-thiolation on Secreted
 Proteins from E. Coli by Mass Spectrometry; Peiran
 Liu²; Malloree Tarnowski¹; Brian Omara²; Wei Wu²;
 Haiying Zhang²; James Tamura²; Michael Ackerman²;

- Li Tao²; Reb Russell²; ¹University of Michigan, Ann Arbor, MI; ²Bristol-Myers Squibb, Pennington, NJ

 ThP 578 Identification and Characterization of Deamidation Sites of Human Growth Hormone; Weidong Cui¹; Chunxiang Yao¹; Tzu-yung Lin¹; Cheng Lin¹; Peter B. O'connor²; ¹Boston University School of Medicine, Boston, MA; ²University of Warwick, Coventry, UK
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- ThP 579 GC-MS/MS Support in the Evaluation of the Toxicokinetics of VX Following Intravenous and Percutaneous Exposures in Minipigs; Jeffrey M.

 Mcguire; Stanley W. Hulet; E. Michael Jakubowski, Jr; Sandra A. Thomson; US Army ECBC, Apg, MD
- ThP 580 Quantification of Benzocaine in Rat Plasma Using UPLC-ES/MS/MS; Kellie Woodling¹; Tong Zhou²; Linda VonTungeln¹; Frederick Beland¹; Kevin Greenlees²; Daniel R. Doerge¹; ¹Nat. Ctr. Tox. Res., Jefferson, AR; ²FDA/Center for Veterinary Medicine, Rockville, MD
- ThP 581 Serum Metabolome and Frontal Cortex Proteome
 Alterations in C57Bl/6 Mice Persist Past
 Withdrawal of Chronic Tobacco Smoke Exposure;
 Rachel Neal; Sadiatu Musah; Robert M. Greene; M
 Michele Pisano; University of Louisville, Louisville, KY
- ThP 582 Quantitative LC/MS Screening for Illicit Drugs in Biological Matrices Using Ultrahigh Resolution

 Mass Analysis and Accurate Mass Confirmation;

 Kevin J. Mchale¹; Mark Sanders²; **Thermo Fisher,
 Somerset, NJ; **Thermo Fisher Scientific, Somerset, NJ
- ThP 583 A Quick LC/MS/MS Method for the Analysis of Common Benzodiazepines and Opiates; Tania A.

 Sasaki¹; Sumandeep Rana²; Wayne B. Ross²; ¹Applied Biosystems, Foster City, CA; ²Redwood Toxicology, Santa Rosa, CA
- ThP 584 Metabonomic Profiling of D-Serine-Induced
 Toxicity Biomarkers in Rat Urine; Rhonda L.
 Pitsch^{1,3}; Claude Grigsby¹; Nicholas DelRaso¹; Louis
 Tamburino²; Mateen Rizki²; John Schlager¹; Pavel
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 WPAFB, OH; ²Wright State University, Dayton, OH;
 ³Henry M. Jackson Foundation, Wright-Patterson AFB,
 OH
- ThP 585 Determination of VX Sequestered Within
 Göttingen® Minipig Skin Following Percutaneous
 Exposure Using LC-MS-MS and GC-MS-MS;
 Jeffrey M. Mcguire; Stanley Hulet; E. Michael
 Jakubowski, Jr; Sandra Thomson; Christopher Byers;
 US Army ECBC, APG, MD
- ThP 586 Performance Evaluation of Three LC-MS Methods Implemented on Ion Trap Mass Spectrometer for Drug Testing in Urine; Guifeng Jiang; Marta Kozak; Subodh Nimkar; Thermo Fisher Scientific, San Jose, CA
- ThP 587 Chemoproteomic Investigation of the Idiosyncratically Hepatotoxic Fluoroquinolone Trovafloxacin; Shaun Mcloughlin; Hua Tang; Paul Richardson; Scott Warder; Jie Lai-Zhang; Michael Liguori; Eric Blomme; Abbott Laboratories, Abbott Park. IL
- ThP 588 Protein profiling Using Tandem Mass Tags to
 Classify Chemical Allergens in Cell Culture Models;
 Petra Budde¹; Hans-dieter Zucht¹; Karsten Kuhn¹; Sasa Koncarevic¹; Christian Baumann¹; Stefan Selzer¹; Lisa Dietz²; Stefanie Ohnesorge²; Herrmann-Josef Thierse²; Peter Schulz-knappe¹; Proteome Sciences R&D GmbH

- & Co. KG, Frankfurt, Germany; ²University Heidelberg, Mannheim, Germany
- ThP 589 Quantitative Proteomic Analysis of HepG2 Cells after Ethanol Exposure; Stanley M. Stevens, Jr.; Robert Buzzeo; Patrick C. Bradshaw; University of South Florida, Tampa, FL
- ThP 590 Quantification of Potential DNA Glycation
 Biomarkers for Diabetes in Biological Samples by
 LC-MS/MS; Hongxia Wang; Huachuan Cao; Yinsheng
 Wang; University of California, Riverside, CA
- ThP 591 LC-MS Detection of 4-ABP-DNA Adduct Formation in Bladder Cells and Tissues; Kristen Randall¹; Dayana Argoti¹; Joseph D. Paonessa²; Yi Ding²; Zachary Oaks¹; Yuesheng Zhang²; Paul Vouros¹; ¹Northeastern University, Boston, MA; ²Roswell Park Cancer Institute, Buffalo, NY
- ThP 592 Sensitive Determination of Hydroxylated-PAHs in Human Urine by Ultra Performance Liquid Chromatography Coupled to Time-of-Flight Mass Spectrometry; Eric Gaudreau; Pierre Dumas; Eric Daigle; Nathalie Morissette; Institut National de Santé Publique du Québec, Québec, Canada
- ThP 593 On Line Sample Extraction Technique vs
 Traditional Sample Preparation Methods for LCMS Toxicology Screening; Marta Kozak; Guifeng
 Jiang; Subodh Nimkar; Thermo Fisher Scientific, San
 Jose, CA
- ThP 594 Serum Metabolite Profiling in the Search for Biomarkers of Inflammation; Erin G. Prestwich; Ramesh Babu Indrakanti; Koli Taghizadeh; Peter Dedon; Massachusetts Inst. of Technology, Cambridge, MA
- ThP 595 Hepatoxicity Biomarkers Found from Coumarin-Treated Rat Liver Tissues Utilizing MALDI TOF and FTMS Imaging Techniques; Lily Li¹; Katherine Kellersberger²; Paul Kowalski²; Jane-Marie Kowalski²; Paul Speir²; David Ho¹; Bob Xiong¹; Patrick Bennett¹; S Stellar³; H.K. Lim³; ¹TandemLabs, Woburn, MA; ²Bruker Daltonics, Billerica, MA; ³Johnson & Johnson, Raritan, NJ
- ThP 596 Robust Differentiation of Isobaric Urine Opioids and n-desmethyl metabolites Using LC-Hybrid Tandem Mass Spectrometry (LC-MSMS) and Automated Library Search; Judy Stone¹; Deborah French^{2,3}; Katherine Chen^{2,3}; Alan Wu^{2,3}; TPMG Regional Laboratories-Northern California, Richmond, CA; ²Univ. of Calif. San Francisco, San Francisco, CA; ³San Francisco General Hospital, San Francisco, CA
- ThP 597 Determination of Arsenic Species in Urine and Serum Samples from Rats Exposed to Arsenite;

 Baowei Chen¹; Anthony McKnight-Whitford¹; Lora L. Arnold²; Shugo Suzuki²; Karen L Pennington²; Samuel M. Cohen²; X. Chris Le¹; ¹University of Alberta, Edmonton, Canada; ²University of Nebraska Medical Center, Omaha, Nebraska
- ThP 598 **Binding of Phenylarsine Oxide to Rat and Human Hemoglobin**; <u>Jie Liu</u>; Chris Le; *University of Alberta*, *Edmonton. Canada*
- ThP 599 Multi Target Screening for 700 Drugs Using a QTRAP LC-MS-MS System and Automated Library Searching; Sebastian Dresen; Nerea Ferreirós Bouzas; Heike Gnann; Wolfgang Weinmann; Institute of Legal Medicine, Freiburg, Germany
- ThP 600 Quantitative Analysis of Bisphenol-A by GC-MS-MS-(NCI) in Biological Liquid Including Urine,

- Blood, Serum/Plasma, Saliva, Milk and Fruit Juice; Pierre Dumas; Éric Daigle; INSPQ, Québec, Canada
- ThP 601 Cardiac Toxicity of 2,3,7,8-Tetrachlorodibenzo-p-Dioxin (TCDD) in Juvenile Zebrafish Heart: Profiling Proteomic Changes by Label Free Quantitation Methods; <u>Lingjun Li</u>; Jiang Zhang; Kevin Lanham; Richard Peterson; Warren Heideman; University of Wisconsin, Madison, WI
- ThP 602 Development of a LC/MS/MS Method for Determining VX Hydrolysis Product EA-2192 Concentration in Biological Matrices Following Exposure; Stanley Hulet; E. Michael Jakubowski, Jr; Sandra Thomson; Ronald Evans; U.S. Army ECBC, APG-EA, MD

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 Simin D. Maleknia; The University of New South,
 Sydney, Australia
- ThP 604 Membrane Introduction Tandem Mass
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 Christopher D. Simpson¹; Michael G. Yost^{1,2}; Erik T.
 Krogh^{3,4}; Christopher G. Gill^{3,4}; ¹University of
 Washington, Seattle, WA; ²PNASH Center, Seattle, WA;
 ³Applied Environmental Research Labs. (AERL),
 Nanaimo, B. C., Canada; ⁴Vancouver Island University,
 Nanaimo, B. C., Canada
- ThP 605 Environmental Quality. Mass spectrometry,
 Olfactometry and Diffusion Modelling to Define Air
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 Davoli¹; Giancarlo Bianchi¹; Marinella Palmiotto¹;
 Giorgio Celeste¹; Roberto Fanelli¹; Elena Fattore¹;
 Massimiliano Il Grande²; Andrea N. Rossi²; ¹Mario
 Negri Institute, Milano, Italy; ²Progress S.r.L., Milano,
 Italy
- ThP 606 A Gas-to-Liquid Membrane Interface for Analysis of Volatile Organics in the Gas Phase by Electrospray Ionization Mass Spectrometry; Eric J Lanni; Mark E. Bier; Carnegie Mellon University, Pittsburgh, PA
- ThP 607 Real-Time *in-situ* Multidimensional Characterization of Ultrafine Diesel Tailpipe Particles Using Single Particle Mass Spectrometry;

 Alla Zelenyuk¹; Dan Imre²; Yong Cai^{1,5}; John M. E. Storey³; Jian Wang⁴; Gunnar Senum⁴; Shean Huff³; Sam Lewis³; Dean Edwards³; ¹Pacific Northwest National Laboratory, Richland, WA; ²Imre Consulting, Richland, WA; ³Oak Ridge National Laboratory, Oak Ridge, TN; ⁴Brookhaven National Laboratory, Upton, NY; ⁵University of Wyoming, Laramie, WY
- ThP 608 Single Particle Mass Analysis for Direct
 Determination of Particle Fluxes in MicroMeteorological Experiments; Klaus-Peter Hinz¹;
 Elmar Gelhausen¹; Bernhard Spengler¹; Andres
 Schmidt²; Otto Klemm²; ¹University of Giessen,
 Giessen, Germany; ²University of Münster, Münster,
 Germany
- ThP 609 Effects of Particle Composition and Morphology on Laser Desorption Ionization Mass Spectra; Joseph P Klems; Murray V. Johnston; University of Delaware, Newark, DE

- ThP 610 Capillary Electrophoresis-Mass Spectrometry: a
 Useful Tool to Distinguish between Weak and
 Strong Organic Acids in Atmospheric Fine
 Particulate Matter; Mahmoud M. Yassine¹; Ewa
 Dabek-Zlotorzynska*¹; Philippe Schmitt-Kopplin²;

 ¹ Analysis & Air Quality, Environment Canada, Ottawa,
 ON; ² Institute of Ecological Chemistry, Neuherberg,
 Germany
- ThP 611 Composition and Yield of Oligomers in Biogenic Secondary Organic Aerosol; Wiley A. Hall; Murray V. Johnston; University of Delaware, Newark, DE
- ThP 612 Reactions of Aliphatic Amines with Ammonium Sulfate Clusters; Bryan R. Bzdek; Murray V. Johnston; University of Delaware, Newark, DE
- ThP 613 Formation and Decomposition of Negative
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- ThP 614 A Robust Bayesian-based Recovery Algorithm for Resolution Enhancement in Time-of-Flight Mass Spectrometry; Robert Jackson; Zhongyu Yang; C. Bronson Crothers; David A. Ferris; Stephen A. Lammert; Stillwater Scientific Instruments, Inc., Orono,
- ThP 615 Micro Array Ion Guide A New Way of Ion Introduction into TOF Mass Spectrometer; Boris Kozlov¹; Andrey Trufanov¹; Dmitriy Alekseev^{1,2}; Mikhail Yavor^{1,2}; Anatoli Verentchikov¹; ¹MS Consulting, Bar, Yugoslavia; ²Institute For Analytical Instrumentation RAS, St. Petersburg, Russia
- ThP 616 A Novel Ion Trap that Enables High Duty Cycle and Wide M/Z-Range on an Orthogonal Injection TOF Mass Spectrometer; Igor Chernushevich; Alexandre Loboda; MDS Analytical Technologies, Concord, ON
- ThP 617 A Gridless Ion Decleration Cell for Improved
 Sensitivity and Ion Yields in Tandem
 Photodissociation Time-of-Flight Mass
 Spectrometry; Kevin Kmiec; Jody May; David H.
 Russell; Texas A&M University, College Station, TX
- ThP 618 MALDI-TOF-TOF with High Resolution Precursor Selection and Multiplexed MS-MS; Kevin Hayden; Stephen C. Gabeler; Mark Dahl; Marvin Vestal; Virgin Instruments Corp., Sudbury, MA
- ThP 619 Time-Resolved Vacuum UV Photodissociation of Peptides in ESI Linear Ion Trap/Orthogonal TOF Mass Spectrometer; Tae-young Kim; James P. Reilly; Indiana University, Bloomington, IN
- ThP 620 Development of an Electron Transfer Dissociation Capable Ultra High Resolution Orthogonal Quadrupole Time of Flight Mass Spectrometer;

 Carsten Stoermer²; Desmond A. Kaplan¹; Ralf Hartmer²; Markus Lubeck²; Oliver Raether³; Melvin A. Park¹; **IBruker Daltonics, inc., Billerica, MA; **2Bruker Daltonik GmbH, Bremen, Germany; **3Bruker Daltonik, Bremen, Germany
- ThP 621 Structural Analysis of Biomolecules Using High-Energy Collision Induced Dissociation in a Multi-Turn Tandem Time-of-Flight Mass Spectrometer "MULTUM-TOF/TOF"; Shuichi Shimma; Ayumi Kubo; Hirofumi Nagao; Michisato Toyoda; Osaka University, Toyonaka, Japan
- ThP 622 A Stigmatic Mass Microscope with a High Mass Resolving Power Using a Multi-Turn Time-of-Flight Mass Spectrometer; <u>Hisanao Hazama</u>^{1,6}; Jun Aoki^{2,6};

- Hirofumi Nagao^{1,6}; Ren Suzuki^{1,6}; Hidetoshi Yoshimura^{1,6}; Yasuhide Naito^{3,6}; Michisato Toyoda^{2,6}; Katsuyoshi Masuda^{4,6}; Kenichi Fujii^{5,6}; Toshio Tashima⁶; Kunio Awazu^{1,6}, ¹ Graduate School of Engineering, Osaka University, Suita, Osaka, Japan; ² Graduate School of Science, Osaka University, Toyonaka, Osaka, Japan; ³ GPI, Hamamatsu, Shizuoka, Japan; ⁴ Suntory Institute for Bioorganic Research, Mishima-gun, Osaka, Japan; ⁵ Osaka Institute of Technology, Hirakata, Osaka, Japan; ⁶ JST, Crest, Chiyoda-ku, Tokyo, Japan
- ThP 623 Characterization of Complex Biological Mixtures
 Using Multi-Reflection TOFMS in Different Mass
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 Joseph, MI; ²Institute of Analytical Instrumentation,
 Saint Petersburg, Russian Federation
- ThP 624 Design, Optimization, and Performance Evaluation of New MALDI-TOF MS and MS-MS Instruments; Marvin Vestal; Virgin Instruments Corp., Sudbury, MA
- ThP 625 A New Multi-Turn Time-of-Flight Mass
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 Nishiguchi¹; Hiroki Sakae¹; Yoshihiro Ueno¹; <u>Kiyoshi</u>
 Ogawa¹; Yoshikazu Yoshida¹; Michisato Toyoda²;
 Mitsutoshi Setou³; *Shimadzu Corporation, Kyoto,
 Japan; *Osaka University, Toyonaka, Osaka, Japan;
 *Hamamatsu University School of Medicine,
 Hamamatsu, Japan
- ThP 626 Determination of the Stability Phase Space of Multi-Turn TOF Using for Imaging Mass Spectrometry; Jun Aoki^{1,6}; Hisanao Hazama^{2,6}; Michisato Toyoda^{1,6}; Kunio Awazu^{2,6}; Katsuyoshi Masuda^{3,6}; Kenichi Fujii^{4,6}; Toshio Tashima⁶; Yasuhide Naito^{5,6}; ¹Graduate School of Science, Osaka University, Toyonaka, Osaka, Japan; ²Graduate School of Engineering, Osaka University, Suita, Osaka, Japan; ³Suntory Institute for Bioorganic Research, Mishima-gun, Osaka, Japan; ⁴Osaka Institute of Technology, Hirakata, Osaka, Japan; ⁵GPI, Hamamatsu, Shizuoka, Japan; ⁶JST, Crest, Chiyoda-ku, Tokyo, Japan
- ThP 627 Maximizing Performance Of Conventional Time-of-Flight Technology: Resolution, Accuracy And Speed; Michael Ugarov; James Bertsch; Bill Barry; John Fjeldsted; Agilent Technologies, Santa Clara, CA
- ThP 628 Improved Resolution and Substantially Higher Sensitivity on a Quadrupole-TOF Mass Spectrometer; Alexandre Loboda; Igor Chernushevich; Nic Bloomfield; MDS Analytical Technologies, Concord, ON
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- ThP 631 Stability of DNA Duplex Containing Hypoxanthine in the Gas Phase Versus Solution Phase; Xuejun Sun; Jeehiun K. Lee; Rutgers University, Piscataway, NJ
- ThP 632 Gas Phase S_N2 Reactions of 1,3-Dimethyluracil and Analogs. Insights into the Mechanism of Uracil Removal by the UDG Enzyme; Anna Zhachkina; Jeehiun K. Lee; Rutgers University, Piscataway, NJ
- ThP 633 Competition between Substitution and Elimination in the Reactions of Dianions with Substituted and Cyclic Alkyl Halides; Keyanna Conner; Renan Joviliano; Andrew Alexander; Scott Gronert; Virginia Commonwealth Univ, Richmond, VA
- ThP 634 Gas Phase Reactions of Alpha Nucleophiles;

 Veronica M. Bierbaum; Stephanie M. Villano; Nicole
 Eyet; W. Carl Lineberger; University of Colorado,
 Boulder, CO
- ThP 635 Gas Phase Anion Chemistry Relevant to the Interstellar Medium; Oscar Martinez Jr. ¹; Brian Eichelberger ¹; Zhibo Yang ¹; Theodore P. Snow ^{1,2}; Veronica M. Bierbaum ¹; ¹University of Colorado, Boulder, CO; ²Center for Astrophysics and Space Astronomy, Boulder, CO
- ThP 636 Charged Carbenes; Fabiane M Nachtigall¹; Yuri E
 Corilo¹; Patrícia Verardi Abdelnur¹; Marcos N Eberlin¹;
 Jairton Dupont²; ¹ThoMSon Lab UNICAMP, Campinas,
 SP, Brazil; ²Laboratory of Molecular Catalysis, Porto
 Alegre, RS, Brazil
- ThP 637 Identification of Aromatic Epoxide Functionalities in Protonated Analytes by Using Ion-molecule Reactions in a Fourier-transform Ion Cyclotron Resonance Mass Spectrometer; Ryan J Eismin; Purdue University, West Lafayette, IN
- ThP 638 Reactivity Studies of Hydroxy-Substituted
 Dehydropyridines; Jennifer Reece¹; Bartłomiej
 Jankiewicz¹; John Nash²; Hilkka Kenttamaa³; ¹Purdue
 University, West Lafayette, IN; ²Department of
 Chemistry, West Lafayette, IN; ³Chemistry Department,
 West Lafayette, IN
- ThP 639 Gas-Phase Ion-Molecule Reactions for the Differentiation of Primary, Secondary and Tertiary Hydroxyl Functionalities in Unknown Protonated Analytes; Mingkun Fu¹; Penggao Duan²; Hilkka Kenttamaa³; ¹Purdue University, West Lafayette, IN; ²Bruker Daltonics, Billerica, MA; ³Chemistry Department, West Lafayette, IN
- ThP 640 Differentiation of Carbohydrate Phosphates and Sulfates by Gas-Phase Ion-Molecule Reactions;

 Matthew Hurt; Yuriy Pyatkivskyy; Victor Ryzhov;

 Northern Illinois University, DeKalb, IL
- ThP 641 **Ion-Neutral Complex Mediated Charge-Transfer Reaction: Gas Phase Fragmentation of Phenyl-, benzenesulfonamides**; Nan Hu¹; Ya-Ping Tu²;
 Yuanjiang Pan¹; Department of Chemistry, Hangzhou,
 China; Genelabs Technologies, Redwood City,
 California
- ThP 642 **Ion-Neutral Complex Resulting from Dissociative Protonation: Fragmentation of α-Furanylmethyl Benzyl Ether**; <u>Pengyuan Liu</u>; Yuanjiang Pan;

 Department of Chemistry, Zhejiang University,

 Hangzhou, China
- ThP 643 Studying the Mechanism of Cysteine S-Nitrosylation by Ion-Molecule Reactions; Victor Ryzhov¹, Richard A. J. O'Hair², Northern Illinois University, DeKalb, IL; ²University of Melbourne, Victoria, Australia
- ThP 644 In-Situ Selective and Sensitive Detection of Monosaccharides by Reactive Desorption

- Electrospary Ionization (DESI) Using Modified Phenylboronic Acids; Yun Zhang¹; Caroline Krieger¹; Dina R. Justes²; Feng Feng¹; Hao Chen¹; ¹Ohio University, Athens, OH; ²Purdue University, West Lafayette, IN
- ThP 645 Ion/Molecule Reactions of Electrogenerated Ions at Atmospheric Pressure; Jiwen Li; Zhixin Miao; Hao Chen: Ohio University. Athens. OH
- ThP 646 Structural Fingerprinting of Recombinant Proteins
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 Ion/Molecule Chemistry; Kevin Turney; Paul Schnier;
 Amgen, Thousand Oaks, CA
- ThP 647 Characterization of PEGs and PEGylated
 Biotherapeutics by ESI Ion-Mobility Time-of-Flight
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 Reactions; Asish Chakraborty; Weibin Chen; John
 Gebler; Waters Corporation, Milford, MA
- ThP 648 A Mechanistic Study of the H/D Exchange of Phenylalanine-Containing Peptides; Laura Simpson; Young Lee; Elaine M. Marzluff; Grinnell College, Grinnell, IA
- ThP 649 A Computational Investigation of the Gas Phase Hydrogen/Deuterium Exchange of Aspartic Acid and Arginine Containing Peptides; Ning-shiuan Lee; Elaine M. Marzluff; Grinnell College, Grinnell, IA
- ThP 650 H/D Exchange and Computational Modeling of Serine-Containing Peptides in the Gas Phase; Maya Lipert; Elaine M. Marzluff; Grinnell College, Grinnell, 14
- ThP 651 Capabilities of High Resolution Laser Ablation Mass Spectrometry to Study Aluminosilicates
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- ThP 652 Energetics of the Formation of Metal Sulfide
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 Calculations; <u>Kaitlin Papson</u>; Jeffrey Spraggins; Una
 Kim; Nicholas Zeringo; Katherine Mullaugh; George
 Luther; Douglas P. Ridge; *University of Delaware*,
 Newark, DE
- ThP 653 Reactivity Comparison of Pd and Pt Catalysts
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 Thota¹; Claude Charvy¹; Denis Lesage¹; Laurent
 Giordano³; Stéphane Humbel³; Anne Milet²; Gérard
 Buono³; Jean-claude Tabet¹; ¹University Paris VI
 (UPMC), Paris Cedex O5, France; ²LEDSS, Chimie
 Recherche UMR 5616, Grenoble, France; ³ECM,
 Faculté St-Jérôme, Marseille, France
- ThP 654 Production of Titanium/Oxygen Cluster Ions by
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 LSMCL Université Paul Verlaine, Metz, France
- ThP 655 Monitoring Gas Phase Ion-Molecule Reactions of
 Environmentally Significant Metal Clusters with
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 Spraggins; Kaitlin Papson; Nicholas Zeringo; Una Kim;
 Katherine Mullaugh; George Luther; Douglas Ridge;
 University of Delaware, Newark, DE
- ThP 656 On Performing Simultaneous ETD/CID on Multiply Protonated Peptides in a Linear Ion Trap; J. Larry Campbell¹; James Hager²; J.c. Yves Leblanc²; ¹MDS

- Analytical Tech, Sciex, Concord, Canada; ²MDS Analytical Technologies, Concord, ON
- ThP 657 Schiff Base Formation in Protonated Peptides via Ion/Ion Reactions in the Gas Phase; Hongling Han; Anastasia Kharlamova; Scott A. McLuckey; Purdue University, West Lafayette, IN
- ThP 658 Charge Inversion Ion/Ion Reactions of
 Corticosteroids: Proton Transfer versus Anion
 Attachment; Kerry Hassell¹; J.c. Yves Leblanc²; Scott
 A. Mcluckey¹; Purdue University, West Lafayette, IN;

 ²MDS Analytical Technologies, Concord, On, ON
- ThP 659 Computational Evidence for Electron Delocalization in Fixed-Charge Tagged Peptide Dications upon Electron Capture and Transfer; Thomas W. Chung; Frantisek Turecek; University of Washington, Seattle, WA
- ThP 660 Electron Induced Fragmentation of β Peptides;

 Hisham Ben Hamidane¹; Aleksey Vorobyev¹; Adrian
 Schmid¹; Maud Larregola²; Aneta Lukaszuk²; Dirk
 Tourwé²; Philippe Karoyan²; Yury O. Tsybin¹; ¹Ecole
 Polytechnique Federale, Lausanne, Switzerland;
 ¹Universite Pierre et Marie Curie, Paris, France

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- ThP 662 **Development of a Bioanalytical Platform for**Supporting High Throughput *in-vitro* Protein
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 Jennifer Maloney; Jeremy Stewart; John Herbst;
 Charlie Conway; Harold Weller; Wilson Shou; Jun
 Zhang; Bristol Myers Squibb, Wallingford, CT
- ThP 663 A highly Automated 5 Pump, 4 Detector Super-Critical Fluid Chromatography Mass Spectrometry (SFC/MS) System for Chiral Purification in Drug Discovery; Qing Ping Han; Mark J. Hayward; Lundbeck Research USA, Paramus, NJ
- ThP 664 A High Throughput On-line SPE-LC-MS/MS
 Method for Quantitative Determination of CVT3619 in Human Urine; Chungwen Chen; Belinda
 Wong; Nevena Mollova; Kwan Leung; CV
 Therapeutics, Inc., Palo Alto, CA
- ThP 665 **High-Throughput Analysis of** *in vivo* **Pharmacokinetic Studies Using Sample Pooling Followed by UPLC-MS/MS**; <u>Jessie Dahlström</u>¹; Tjerk

 Bueters¹; Ingvar Betnér²; Sveinn Briem¹; ^IAstrazeneca

 R&D, Södertälje, Sweden; ²Waters, Sollentuna, Sweden
- ThP 666 UPLC-MS/MS in High-Throughput Detection,
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 Steroids in Equine Plasma; Youwen You¹; Fuyu
 Guan¹; Xiaoqing Li¹; Cornelius Uboh^{1,2}; Lawrence
 Soma¹; Jeffrey Rudy²; Jinwen Chen¹; Ying Liu¹;

 ¹University of Pennsylvania, West Chester, PA; ²PA
 Equine Toxicology, West Chester, PA
- ThP 667 Throughput Advantages of Two-Dimensional
 Chromatography with Multiple Parallel LC Systems
 Utilizing a Single Data File; Matthew Berube; Thermo
 Fisher Scientific, Franklin, MA
- ThP 668 Simple and Rapid Screening of Melamine in Milk Products with High Resolution Accurate Mass Bench Top Orbitrap LCMS; Kefei Wang; Chunang (christine) Gu; Jie Qian; Ze Zhang; James chang; ThermoFisher Scientific, San Jose, CA

- ThP 669 Label Free High-Throughput Whole Protein Kinase Screening Assay; Michelle V. Romm¹; Nikunj Parikh¹; Thomas B. Stanley²; Jon D. Williams²; William A. Lamarr¹; Can "jon" Ozbal¹; ¹BioTrove, Inc., Woburn, MA; ²GlaxoSmithKline, Research Triangle Park, North Carolina
- ThP 670 High Throughput Quantitative Sample Analysis
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 Combined with On-Line SPE; Min J. Yang; David M.
 Cox; Adrian Taylor; Peter Kovarik; John Gibbons;
 MDS Analytical Technologies, Concord, Canada
- ThP 671 A High Throughput 10-in-1 LC/MS/MS Method to Support CYP Inhibition Studies Using Human Liver Microsomes; Dandan Wang; Jianrong Lin; Diansong Zhou; Connie Azumaya; Scott Grimm; AstraZeneca Pharmaceuticals LP, Wilmington, DE
- ThP 672 Automated Peptide Mapping: Digestion, LC-MS, and Data Analysis; Jason L. Richardson; Bhavana Shah; Pavel V. Bondarenko; Gang Xiao; Zhongqi Zhang; Amgen, Inc., Thousand Oaks, CA
- ThP 673 A High Speed High Resolution Open Access Multi Column LCMS System for Diverse Application Needs; Oliver Keil¹; Michael Frank²; Angelika Gratzfeld-Huesgen²; ¹Graffinity Pharmaceuticals, Heidelberg, Germany; ²Agilent Technologies, Waldbronn, Germany
- ThP 674 High Throughput Screening of Deoxynivalenol by MALDI-TOF Mass Spectrometry; Chang-nan Chen¹; Mei-wun Lin¹; Jentaie Shiea²; ¹Chaoyang University of Technology, Taichung, Taiwan; ²National Sun Yeh-sen University, Kaohsiung, Taiwan
- ThP 675 Improvements in Mass-Directed Preparative HPLC Fractionation to Support Late Stage Lead Optimization; Yinong Zhang; Rongda Xu; Catherine Pham; Lu Zeng; Daniel B. Kassel; Takeda San Diego, Inc., San Diego, CA
- ThP 676 Maximizing Versatility of an Automated Mass
 Directed Preparative HPLC for Multiple Uses and
 Diverse Loading Scales; Leonard Hargiss¹; Philip E
 Keyes¹; Julita Cicogna²; Timothy Stanoch⁴; Trevor
 Cornell³; **ILexicon Pharmaceuticals, Princeton, NJ;
 **Taylor Technologies, Princeton, NJ; **The College of
 New Jersey, Ewing, NJ; **Stevens Institute of
 Technology, Hoboken, NJ
- ThP 677 Discovery of Novel Inhibitors of Serine
 Palmitoyltransferase (SPT) by Mass SpectrometryBased High-Throughput Screening (HTS); Pete
 Meyn¹; Paul Maresca¹; William A. Lamarr²; Peter
 Rye²; Maureen Brooks¹; Adam Babbs³; Martin
 Procter³; David Pan³; Can "Jon" Ozbal²; Andrew
 Garton¹; ¹OSI Pharmaceuticals, Farmingdale, NY;
 ²BioTrove, Inc., Woburn, MA; ³Prosidion Limited,
 Oxford, UK
- ThP 678 Novel Ultra-High-Pressure Splitless Dual Channel Nano-UPLC System for Drastic Increase in Through-Put, Resolution and Sensitivity in Drug and Proteomic Analysis; Frank Yang¹; Austin Yang²; Frank Wu¹; Angel Wu¹; Cathy Chang¹; ¹CVC Technologies, Inc., Vista, USA; ²University of Maryland, Greenbaum Cancer Center, Baltimore,
- ThP 679 Evaluation of New Version DiscoveryQuantTM
 Software for Automated MRM Generation and
 Quantitation for *in vitro* ADME Screening; <u>Haiqing</u>
 <u>Hu</u>¹; Erika Manyak¹; Steven Ainley²; Kevin Shirey²;

- Michael Rooney¹; ¹AstraZeneca R&D Boston, Waltham, MA; ²Sound Analytics, LLC, Niantic, CT
- ThP 680 Cross Platform MS/MS Method Development,
 Transfer and Implementation Using
 DiscoveryQuant Software; Kevin Whalen; Emily
 Hudson; Lisa Buchholz; Sarah Osgood; Pfizer Global R
 & D, Groton, CT
- ThP 681 Co-Polymer Characterization Using Automated On-Line SEC-Pyrolysis GCMS; Junko Iida¹; Erwin Kaal^{2,3}; Hans-Gerd Janssen^{2,4}; ¹Shimadzu Europa GmbH, Duisburg, Germany; ²van't Hoff Institute for Molecular Sciences, Amsterdam, The Netherlands; ³Atas GL International, Veldhoven, The Netherlands; ⁴Unilever Research and Development, Vlaardingen, The Netherlands
- ThP 682 Using Discovery Quant® and Global MS/MS database to facilitate the LC/MS/MS analysis of Discovery In Vitro Protein Binding Assays; Emily Hudson¹; Kevin Whalen²; Erik A. Soderstrom³; Brian Rago¹; Amanda King-ahmad¹; John Janiszewski⁴; Lisa Buchholz⁵; ¹Pfizer, Groton, CT; ²Pfizer Inc, Groton, CT; ³Pfizer, Inc., Groton, CT; ⁴Pfizer Inc., Westerly, RI; ⁵Pfizer Global R & D, Groton, CT
- ThP 683 Fast Analysis of Vitamins in Dietary Supplements
 Using LCMS; Masatoshi Takahashi²; William A
 Hedgepeth¹; Yuhui Wang¹; ¹Shimadzu Scientific
 Instruments, Inc, Columbia, MD; ²Shimadzu, Columbia,
- ThP 684 High Throughput Nanospray Chip for Robust
 Molecular ID Using Direct Infusion; Katherine
 Heaton; Arthur Fogiel; Lee Heineman; Arthur Fogiel,
 Jr; Sau Lan Tang Staats; Phoenix S & T, Inc, Chester,
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- ThP 685 Application of Ultra-Fast LC-MS/MS to High
 Throughput in vivo PK Screening –Techniques to
 Minimize Matrix Effects; Bernard K. Choi; Haiping
 Wang; Gino M. Salituro; Karen Owens; Lucinda
 Cohen; Merck Research Laboratory, Rahway, NJ
- ThP 686 Plasma and Brain Homogenate Sample Pooling on a Hamilton Liquid Handling Robotic System; Joyce Shuman; Bernard Choi; Karen Owens; Gino M. Salituro; Lucinda Cohen; Merck & Co., Inc., Rahway,
- ThP 687 High Throughput Workflow for Midazolam and 1-Hydroxymidazolam Analysis in Human Plasma; Michael Coyer¹; Patrice Tremblay²; Pierre Picard²; Lynn Jordan³; John Siira³; ¹Northern Tier Research, Mayfield, PA; ²Phytronix Technologies, Quebec, QC; ³Caliper Life Sciences, Hopkinton, MA
- ThP 688 A Vortex Cooled Sample Handling and Processing System for Automated H/D Exchange Mass Spectrometry; Yong Chen; Ansgar Brock; Novartis-GNF, San Diego, CA
- ThP 689 Coupling of a Capillary Scale Immobilized Enzyme
 Reactor with Bioextraction/Tandem Mass
 Spectrometry for Identification of Enzyme
 Inhibitors in Mixtures; Erica M Forsberg; John D
 Brennan; McMaster University, Hamilton, Canada
- ThP 690 Validation of Pioglitazone in Human Serum by Two Sample Introduction Methods: LDTD-APCI/MS/MS and LC-ESI/MS/MS; Michael Pugh; Rachel Sun; John W. Torchia; Donald Gray; Brian Engel; BASi, West Lafayette, IN
- ThP 691 Pushing the Envelope on LC/MS Separation Speed: "Knowing When to Push it and When to Back Off";

- Mark J. Hayward; Lundbeck Research USA, Paramus, N.J.
- ThP 692 Evaluation of Protein Precipitation Filter Plates for High-Throughput LC-MS Biological Sample Preparation; Lan Gao; Meng Xu; Swapan Chowdhury; Schering-Plough, Kenilworth, NJ
- ThP 693 Multi-Adsorption Reverse SPE to Clean up Bioanalytical Samples for LC-MS; <u>Jerry Wang</u>; Jerry Wang; <u>Agela Technologies Inc</u>, <u>Newark</u>, <u>DE</u>
- ThP 694 Urinary Metabolite Profiling Using Solid-Phase Extraction and Direct Infusion Electrospray Ionization Fourier Transform Ion Cyclotron Resonance Mass Spectrometry; Bo Blanckenburg; Yuri E.M. van der Burgt; André M. Deelder; Magnus Palmblad; Leiden University Medical Ce, Leiden, Netherlands
- ThP 695 Integrated Workflow to Design Methods and Analyze Data in Large-to-Extremely-Large Scale SRM Experiments; Amol Prakash¹; Reiko Kiyonami¹; Alan E. Schoen²; Huy Nguyen²; Scott Peterman²; Andreas F Huhmer²; Mary F Lopez¹; Bruno Domon³; IntermoFisher Scientific, Cambridge, MA; Thermo Fisher Scientific, San Jose, CA; ETH Zurich, Zurich, Switzerland
- ThP 696 Approaching Real-Time Protein Identification from Mass Spectrometry Data; Joel Coburn¹; Nuno Bandeira²; Pavel Pevzner¹; Vineet Bafna¹; Natalie Castellana¹; Rajesh K. Gupta¹; Kirby Collins³;

 ¹University of California, San Diego, La Jolla, CA;

 ²Center for Computational Mass Spectrometry, UCSD, La Jolla, CA;

 ³Convey Computers, Richardson, TX